GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 23:39:01 ; Search time 8388.21 Seconds
(without alignments)
11011.138 Million cell updates/sec

Title: US-09-856-681A-1
Perfect score: 3093
Sequence: 1 atgaggtcagaagccttgct.....ccaatgatgcgtgtacataa 3093

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3089.8	99.9	6875	11	BC032619	BC032619 Homo sapi
2	1439.4	46.5	3226	11	AK042751	AK042751 Mus muscu
3	1437.6	46.5	3329	11	AK082711	AK082711 Mus muscu
4	1065.8	34.5	2411	14	CB605722	CB605722 AMGNNUC:M
5	899.4	29.1	1030	12	BM450002	BM450002 AGENCOURT
6	896	29.0	1183	12	BM546059	BM546059 AGENCOURT
7	828.2	26.8	868	9	AU140366	AU140366 AU140366
8	813.8	26.3	891	13	BU186963	BU186963 AGENCOURT
9	784.4	25.4	887	12	BG769297	BG769297 602742838
10	783.4	25.3	1201	9	AL543344	AL543344 AL543344
11	779.4	25.2	848	13	BQ678536	BQ678536 AGENCOURT
12	772.4	25.0	883	13	BU172225	BU172225 AGENCOURT
13	770	24.9	864	13	BQ440312	BQ440312 AGENCOURT
14	767.4	24.8	874	13	BU838082	BU838082 AGENCOURT
15	760.6	24.6	890	13	BQ683009	BQ683009 AGENCOURT
16	757.4	24.5	953	13	BU854884	BU854884 AGENCOURT
17	757	24.5	851	14	CD653925	CD653925 AGENCOURT
18	734	23.7	952	13	BU855855	BU855855 AGENCOURT
19	713.8	23.1	835	12	BG477592	BG477592 602522430
20	698.4	22.6	826	14	CD654452	CD654452 AGENCOURT
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22	681.8	22.0	3921	11	AK084922	AK084922 Mus muscu
23	680.2	22.0	4476	11	AK052232	AK052232 Mus muscu
24	670.2	21.7	716	10	BF970807	BF970807 602271438
25	669.4	21.6	802	14	CD653501	CD653501 AGENCOURT
26	668.4	21.6	805	14	CD656935	CD656935 AGENCOURT
27	667	21.6	890	13	BU856543	BU856543 AGENCOURT
28	664.8	21.5	736	10	BE277845	BE277845 601120064
29	660.4	21.4	794	10	AW954605	AW954605 EST366675
30	656.2	21.2	823	12	BG327694	BG327694 602426690
31	645.8	20.9	651	9	AL602452	AL602452 DKFZp686M
32	636.6	20.6	643	10	BE408781	BE408781 601303483
33	631.8	20.4	685	10	BE265000	BE265000 601193829
34	629.8	20.4	703	10	BE384511	BE384511 601277886
35	615.2	19.9	926	12	BG326467	BG326467 602425312
36	614.4	19.9	746	13	BQ770491	BQ770491 UI-M-FI0-
37	614.4	19.9	795	14	CB245479	CB245479 UI-M-FY0-
38	612.2	19.8	772	13	BQ425051	BQ425051 AGENCOURT
39	611.8	19.8	895	12	BI819955	BI819955 603035314
40	608.8	19.7	777	13	BU708565	BU708565 UI-M-FI0-
41	608.6	19.7	747	14	CF535602	CF535602 UI-M-GH0-
42	604.4	19.5	771	14	CA513024	CA513024 UI-R-FJ0-
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44	589.2	19.0	690	12	BG333712	BG333712 602460715
c 45	588.8	19.0	592	14	CA337090	CA337090 NISC_1v09

ALIGNMENTS

RESULT 1
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LOCUS BC032619 6875 bp mRNA linear HTC 04-MAR-2003
DEFINITION Homo sapiens, similar to sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, clone IMAGE:5578066, mRNA.
ACCESSION BC032619
VERSION BC032619.1 GI:22749800
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6875)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 69 Row: o Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11991659
This clone has the following problem: retained intron.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5578066"
/tissue_type="Skin, melanotic melanoma."

/clone_lib="NIH_MGC_72"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 99.9%; Score 3089.8; DB 11; Length 6875;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3091; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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Db        972 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 1031

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
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Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
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Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
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Db       1212 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 1271

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
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Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
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Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
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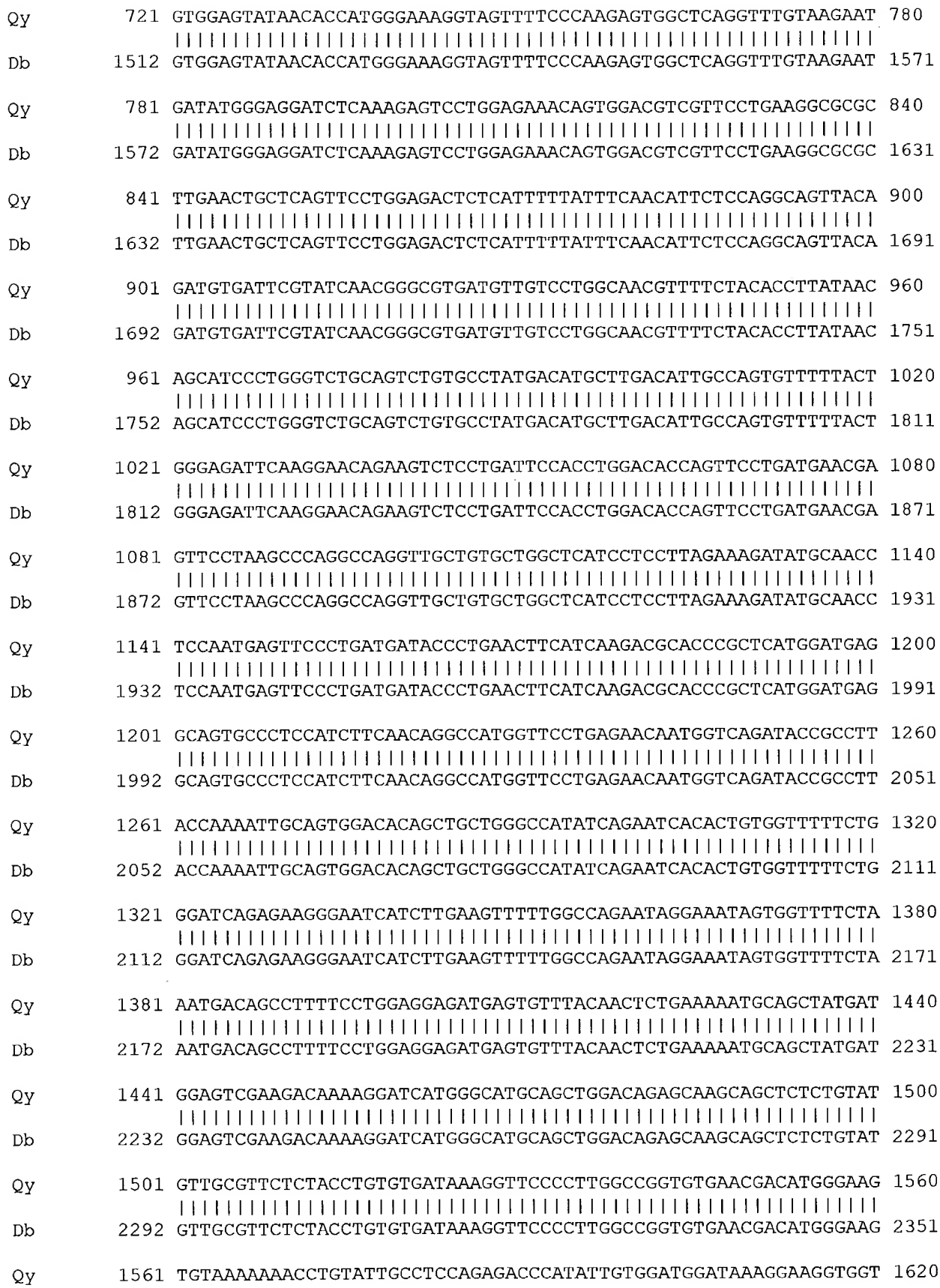

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Qy       2521 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2580
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Qy       2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC 2820
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Qy       3001 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3060
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RESULT 2
AK042751
LOCUS AK042751 3226 bp mRNA linear HTC 19-SEP-2003
DEFINITION Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730020P05 product:sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, full insert sequence.
ACCESSION AK042751
VERSION AK042751.1 GI:26335300
KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3226)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3226
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A730020P05"
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CDS 671. .2488
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ORIGIN

Query Match 46.5%; Score 1439.4; DB 11; Length 3226;
Best Local Similarity 89.1%; Pred. No. 0;
Matches 1554; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db        671 ATGCGGCCAGCAGCCTTACTGCTGTGTCTCACACTGCTACACTGCGCTGGGGCTGGTTTC 730

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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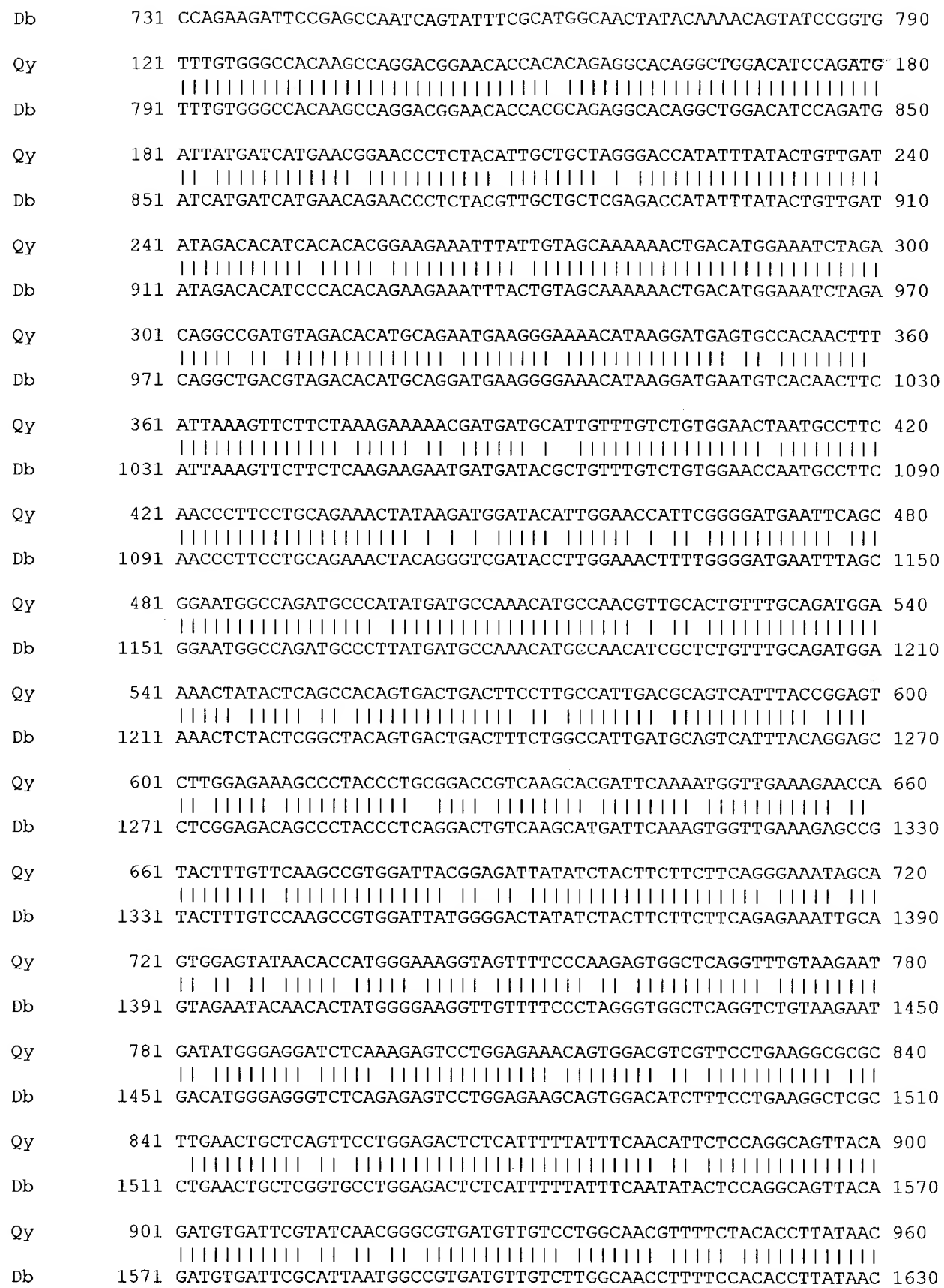

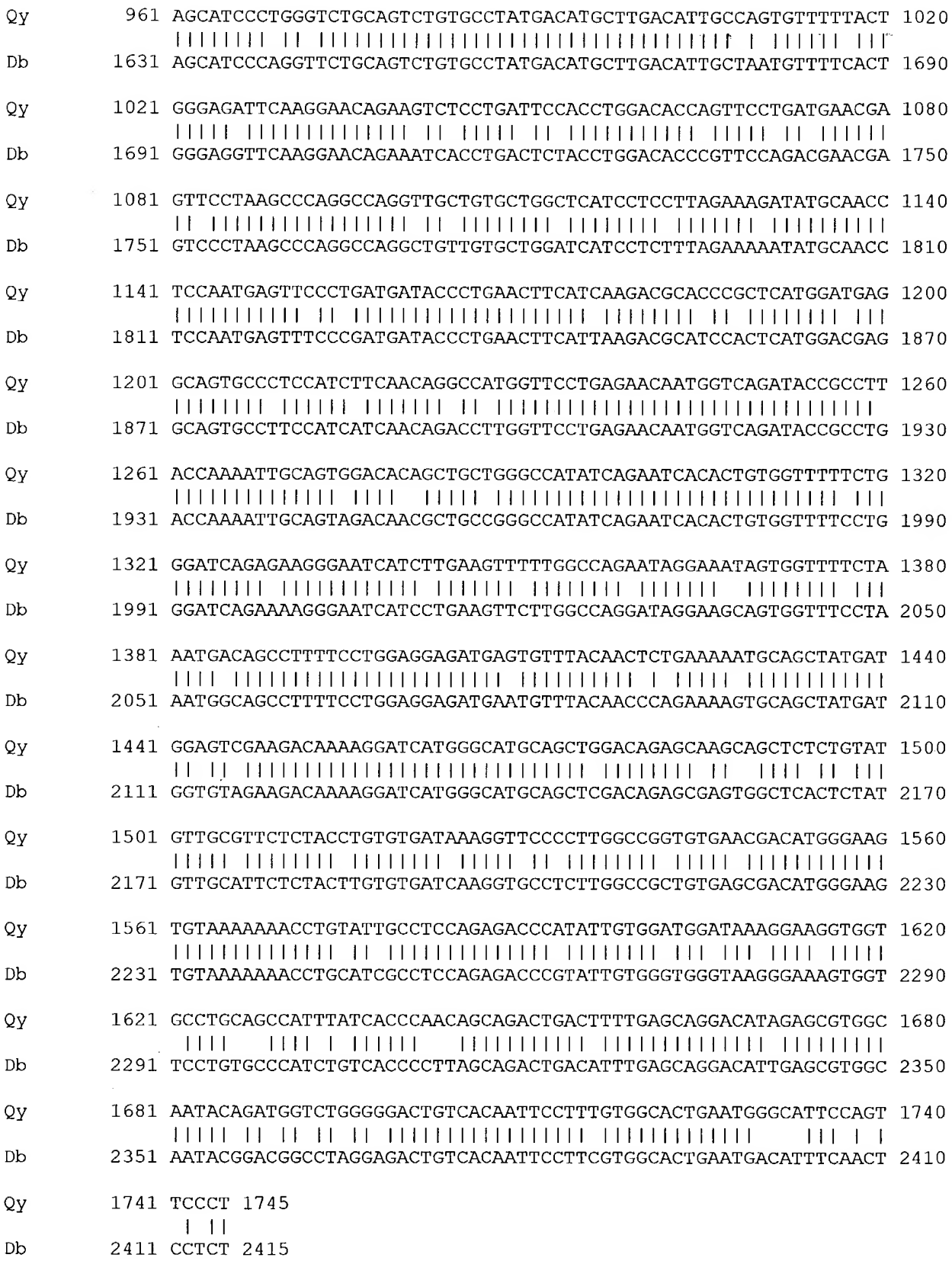

RESULT 3
AK082711
LOCUS AK082711 3329 bp mRNA linear HTC 20-SEP-2003
DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230094A19 product:sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, full insert sequence.
ACCESSION AK082711
VERSION AK082711.1 GI:26349884
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3329)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,

Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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ORIGIN

Query Match 46.5%; Score 1437.6; DB 11; Length 3329;
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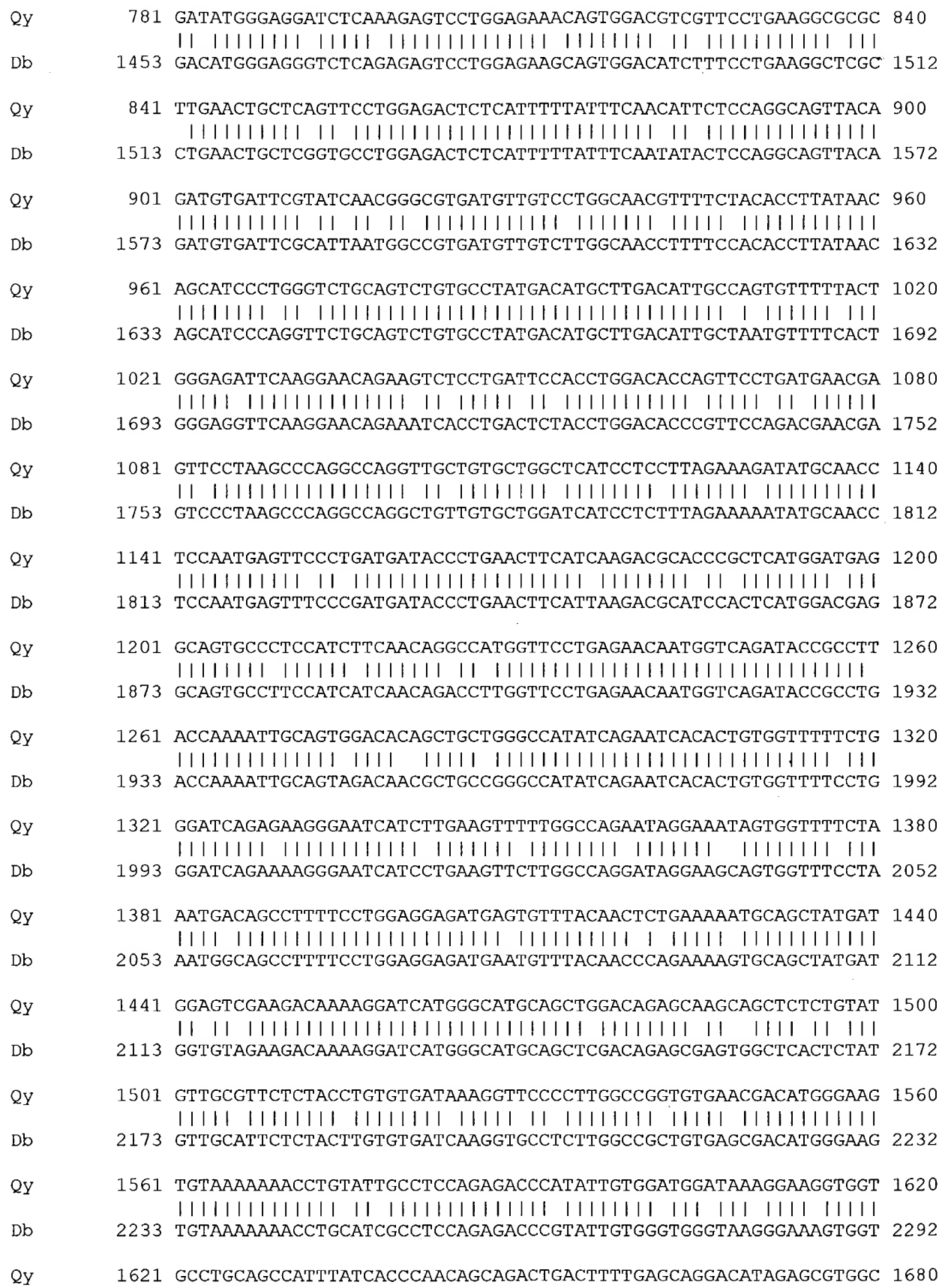

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REFERENCE   1  (bases 1 to 2411)
  AUTHORS   Amgen EST Program.
  TITLE     Amgen Rat EST Program
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Dan Fitzpatrick
            Amgen, Inc
            One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
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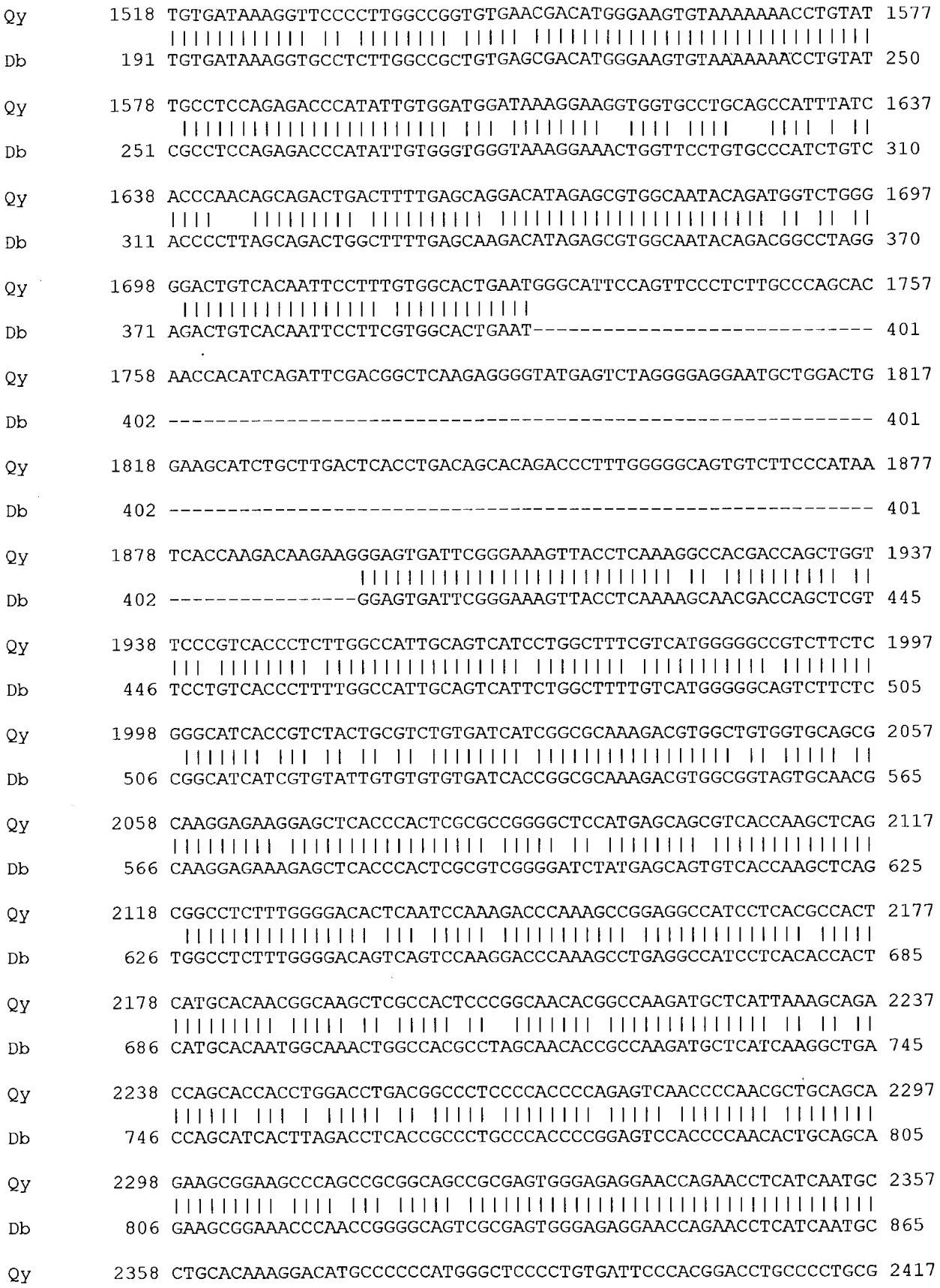

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REFERENCE   1  (bases 1 to 1030)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
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             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
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ORIGIN

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Db        961 TTCCCTCTTGCCCAGNACAAAC 982
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RESULT 6
BM546059
LOCUS BM546059 1183 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6497880 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588479

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            5', mRNA sequence.
ACCESSION   BM546059
VERSION     BM546059.1  GI:18778712
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1183)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12359  row: k  column: 08
            High quality sequence stop: 725.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_125"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."
ORIGIN
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Query Match 29.0%; Score 896; DB 12; Length 1183;
Best Local Similarity 99.0%; Pred. No. 1.5e-201;
Matches 932; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

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Qy       2152 AAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAAC 2211
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Db         18 ATGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAAC 77

Qy       2212 ACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACC 2271
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Db         78 ACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACC 137

Qy       2272 CCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGG 2331
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Db        138 CCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGG 197
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Qy       2332 GAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCT 2391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 GAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCT 257

Qy       2392 GTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTC 2451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 GTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTC 317

Qy       2452 CTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAG 2511
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        318 CTGCCCATCACGCAGCAGGGCTACCAGCACGAGTACGTGGACCAGCCCAAAATGAGCGAG 377

Qy       2512 GTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAA 2571
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Db        378 GTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAA 437

Qy       2572 CATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTG 2631
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Db        438 CATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTG 497

Qy       2632 CCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAG 2691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 CCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAG 557

Qy       2692 ACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAG 2751
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Db        558 ACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAG 617

Qy       2752 AGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAAC 2811
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        618 AGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGNCACCACTCTCAAAAGAAAC 677

Qy       2812 AACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGAC 2871
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Db        678 AACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGAC 737

Qy       2872 AACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCT 2931
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Db        738 AACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCT 797

Qy       2932 GGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGG 2991
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        798 GGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAAG 857

Qy       2992 TC-GGGGCTGAAGCGTACG-CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTG 3049
             || |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        858 TCGGGGGCTGAAGCGTACGCCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTG 917

Qy       3050 CTCCCCTTTCCACATCCATG-AAGCCCAATGATGCGTGTAC 3089
              ||||||||| |||||||||| |||||| ||||||||||||
Db        918 CTCCCCTTTTCACATCCATGAAAGCCCCATGATGCGTGTAC 958
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RESULT 7
AU140366
LOCUS AU140366 868 bp mRNA linear EST 05-AUG-2002

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DEFINITION  AU140366 PLACE2 Homo sapiens cDNA clone PLACE2000407 5', mRNA
            sequence.
ACCESSION   AU140366
VERSION     AU140366.1  GI:11001887
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 868)
  AUTHORS   Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T.,
            Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y. and Isogai,T.
  TITLE     HRI human cDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii,S.,
            Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S.,
            Masuho,Y., Isogai,T.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             26.8%;  Score 828.2;  DB 9;  Length 868;
  Best Local Similarity   98.3%;  Pred. No. 1.7e-185;
  Matches  855;  Conservative    0;  Mismatches   13;  Indels    2;  Gaps    2;

Qy        368 TTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTCAACCCTT 427
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Db          1 TTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTCAACCCTT 60

Qy        428 CCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGCGGAATGG 487
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Db         61 CCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGCGGAATGG 120

Qy        488 CCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGAAAACTAT 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGAAAACTAT 180

Qy        548 ACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGTCTTGGAG 607
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Db        181 ACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGTCTTGGAG 240
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Qy        608 AAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCATACTTTG 667
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCATACTTTG 300

Qy        668 TTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCAGTGGAGT 727
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Db        301 TTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCAGTGGAGT 360

Qy        728 ATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAATGATATGG 787
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Db        361 ATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAATGATATGG 420

Qy        788 GAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGCTTGAACT 847
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Db        421 GAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGCTTGAACT 480

Qy        848 GCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACAGATGTGA 907
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTCAGTTCCTGGAAACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACAGATGTGA 540

Qy        908 TTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAACAGCATCC 967
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Db        541 TTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAACAGCATCC 600

Qy        968 CTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACTGGGAGAT 1027
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Db        601 CTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACTGGGAGAT 660

Qy       1028 TCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGAGTTCCTA 1087
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Db        661 TCAAGGAACAGAAGTCTNCTGATTCCACCTGGACACCAGTTCCTGATGAACGAGTTCCTA 720

Qy       1088 AGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACCTCCAATG 1147
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Db        721 AGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTNCTTAGAAAGATATGCAACCTTCAATG 780

Qy       1148 AGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAGGCAGTGC 1207
              |||||||||||||| ||||||||| |||||||||||||| ||||||||| ||| |||
Db        781 AGTTCCCTGATGAT-CCCTGAACTTNATCAAGACGCACCCGTTCATGGATGA-GCAATGC 838

Qy       1208 CCTCCATCTTCAACAGGCCATGGTTCCTGA 1237
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Db        839 CCTTCATTTTNAACAGGGCATGGGTNCTGA 868
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RESULT 8
BU186963
LOCUS       BU186963                 891 bp    mRNA    linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_7785723 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6138529
            5', mRNA sequence.
ACCESSION   BU186963
VERSION     BU186963.1  GI:22700947
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 891)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13454  row: b  column: 02
            High quality sequence stop: 677.
FEATURES             Location/Qualifiers
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                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.75 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             26.3%;  Score 813.8;  DB 13;  Length 891;
  Best Local Similarity   97.3%;  Pred. No. 4.5e-182;
  Matches  860;  Conservative    0;  Mismatches   18;  Indels    6;  Gaps    3;

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Db          8 TCCGCACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATT 67

Qy       1006 GCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCA 1065
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Db         68 GCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCA 127

Qy       1066 GTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTA 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 GTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTA 187

Qy       1126 GAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCAC 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 GAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCAC 247

Qy       1186 CCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATG 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 CCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATG 307

Qy       1246 GTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCAC 1305
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Db        308 GTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCAC 367

Qy       1306 ACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGA 1365
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Db        368 ACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGA 427

Qy       1366 AATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAA 1425
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Db        428 AATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAA 487

Qy       1426 AAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCA 1485
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Db        488 AAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCA 547

Qy       1486 AGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGT 1545
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Db        548 AGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGT 607

Qy       1546 GAACGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGG 1605
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Qy       1606 ATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAG 1665
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Db        668 ATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAG 727

Qy       1666 GACATAGAGCGTGGCAATACAGAT-GGTCTGGGGGACTGTCACAATTCCTTTGTGGCACT 1724
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Db        728 GACATAGAGCGTGGCAATACAGATGGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACT 787

Qy       1725 GAATGGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGA 1784
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Db        788 GAATGGGCATTCCAGTTCCCTCTTGCCCAGCAC-ACCACATCAGATTCACGGCTCAANGA 846

Qy       1785 GGGGTATGA----GTCTAGGGGAGGAATGCTGGACTGGAAGCAT 1824
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Db        847 AGGGTATGAAGTCCTAAGGGGAGGAAATGCTGGACTGGAAGCAT 890
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RESULT 9
BG769297
LOCUS       BG769297                887 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602742838F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4872704 5',
            mRNA sequence.
ACCESSION   BG769297
VERSION     BG769297.1  GI:14079950
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 887)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
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Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1749 row: k column: 09
High quality sequence stop: 862.

FEATURES Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
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/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 25.4%; Score 784.4; DB 12; Length 887;
Best Local Similarity 95.8%; Pred. No. 4.4e-175;
Matches 849; Conservative 0; Mismatches 31; Indels 6; Gaps 4;

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Db          2 CGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCA 61

Qy       1963 GTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGT 2022
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Db         62 GTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGT 121

Qy       2023 GATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCG 2082
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Qy       2083 CGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCC 2142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCC 241

Qy       2143 AAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACT 2202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2203 CCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCC 2262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCC 361
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Qy       2263 CTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGC 2322
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Db        362 CTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGC 421

Qy       2323 CGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATG 2382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 CGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATG 481

Qy       2383 GGCTCCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGC 2442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GGCTCCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGC 541

Qy       2443 GTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAA 2502
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Db        542 GTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGGCCAAA 601

Qy       2503 ATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAA-GAC 2561
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Db        602 ATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGGAC 661

Qy       2562 CATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCAT-GGGGTGAACCTTGTGGAGAACC 2620
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Db        662 CATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGGTGAACCTTGTGGAGAACC 721

Qy       2621 TGGACAGCCTGCCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGA--GC 2678
              |||||||||||||||| |   | |||||||||||||||||||||| |||| |   |
Db        722 TGGACAGCCTGCCCCCCGATAGTTCACAGCGGGAGGCCTCCCTGGGTCCACCGGTAAGCC 781

Qy       2679 CTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGG 2738
                ||   ||| |||||||||||||||||||||||| ||||||||||||||||||  |
Db        782 TCCCTGTTCTTAGACCGGTCTAAGCAAGCGGCTGGAATTGCACCACTCCTCTTCCTAACG 841

Qy       2739 GGTT--GACTATAAGAGGAGCTACCCCACGAACTCGCTCACGAGAA 2782
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Db        842 GGGTAGACTTATAAGAGGAGCTAACCAAGGAATCGGTTCAAGAGGA 887
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RESULT 10
AL543344
LOCUS       AL543344                1201 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  AL543344 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI001YL17 5-PRIME, mRNA sequence.
ACCESSION   AL543344
VERSION     AL543344.2  GI:31265191
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12875822.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2864.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI001CF09QP1&cluster=2864.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI001CF09QP1.

FEATURES Location/Qualifiers
source 1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DI001YL17"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 25.3%; Score 783.4; DB 9; Length 1201;
Best Local Similarity 96.4%; Pred. No. 9.1e-175;
Matches 838; Conservative 5; Mismatches 21; Indels 5; Gaps 4;

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Qy       1714 TTTGTGGCACTGAATGGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCG 1773
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Qy       1774 ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC 1833
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Db        281 ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC 340

Qy       1834 TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG 1893
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Db        341 TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG 400

Qy       1894 GGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG 1953
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Db        401 GGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG 460

Qy       1954 GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC 2013
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Db        461 GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC 520

Qy       2014 TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC 2073
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Qy       2074 ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGAC 2133
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Db        581 ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGAC 640

Qy       2134 ACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAG 2193
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Db        641 ACTCAATCCAAAGACCCAAAGCCGGAGG-CATCCTCACGCCACTCATGCACAACGGCAAG 699

Qy       2194 CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGAC 2253
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Db        700 CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGAC 759

Qy       2254 CTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC 2313
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Qy       2314 CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG 2373
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Qy       2494 CAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAG 2553
                 || |||||||||||||| ||||||||||||||:|:||||| ||:||||||||||
Db       1000 --AGCCCAAATGAGCGAGGTGG-CCAGATGGCGCTGGARGRCCAGG-CGSCACACTGGAG 1055

Qy       2554 TATAAGACCATCAAGGAACATCTCAGCAG 2582
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Db       1056 TWTAAGACATCAAGGAAATTYAGCAGCAG 1084
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RESULT 11
BQ678536
LOCUS       BQ678536                 848 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8208159 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6262572
            5', mRNA sequence.
ACCESSION   BQ678536
VERSION     BQ678536.1  GI:21791215
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2425  row: b  column: 13
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High quality sequence stop: 695.

FEATURES Location/Qualifiers

source 1. .848
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6262572"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 25.2%; Score 779.4; DB 13; Length 848;
Best Local Similarity 98.1%; Pred. No. 6.6e-174;
Matches 830; Conservative 0; Mismatches 12; Indels 4; Gaps 4;

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Qy       1286 CTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 1345
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Db          1 CTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 60

Qy       1346 AGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA 1405
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Db         61 AGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA 120

Qy       1406 TGAGTGTTTACAACTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG 1465
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Qy       1466 GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA 1525
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Qy       1526 AGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCA 1585
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Qy       1706 ACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACAT 1765
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Qy        1946 CCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCA 2005
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Db         661 CCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCA 720

Qy        2006 CCGTCTACTGCGTCTGTGATCATCGGCGCAAAGA-CGTGGCTGTGGTGCAG-CGCAAGGA 2063
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Db         721 CCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACCGTGGCTGTGGTGCANCCGCAAGGA 780

Qy        2064 GAAGGAGCTCACCCACT-CGCGCCGGGGGCTCCATGAG-CAGCGTCACCAAGCTCAGCGGC 2121
                || |||||||||||||| ||||| |||||| |||||| ||||||||||||||   | |
Db         781 AAAAGAGCTCACCCACTCCGCGCGGGGGCTTCATGAGCCAGCGTCACCAAGCTTCACCGG 840

Qy        2122 CTCTTT 2127
                | || |
Db         841 CCCTCT 846
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RESULT 12
BU172225
LOCUS       BU172225                883 bp    mRNA    linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_7962341 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6106551
            5', mRNA sequence.
ACCESSION   BU172225
VERSION     BU172225.1  GI:22686209
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 883)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2347  row: m  column: 16
            High quality sequence stop: 606.
FEATURES             Location/Qualifiers
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/clone_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 25.0%; Score 772.4; DB 13; Length 883;
Best Local Similarity 98.6%; Pred. No. 3.1e-172;
Matches 779; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy       1361 TAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACT 1420
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Qy       1421 CTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACA 1480
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Qy       1481 GAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCC 1540
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Qy       1781 AAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTG 1840
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Db        494 AAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTG 553
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Qy       1841 ACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGA 1900
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Qy       1961 CAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCT 2020
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Qy       2021 GTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACT 2080
             |||||||||||||||| |||||||||||||  ||| ||||||||||||||||||||
Db        734 GTGATCATCGGCGCAAAAACGTGGCTGTGGTGCCCCGCCAGGAGAAGGAGCTCACCCACT 793

Qy       2081 CGCGCCGGGG 2090
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Db        794 CGCGGCCGGG 803
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RESULT 13
BQ440312
LOCUS       BQ440312                 864 bp    mRNA    linear   EST 24-MAY-2002
DEFINITION  AGENCOURT_7902718 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6157758
            5', mRNA sequence.
ACCESSION   BQ440312
VERSION     BQ440312.1  GI:21179388
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 864)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13504  row: c  column: 07
            High quality sequence stop: 659.
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN

Query Match 24.9%; Score 770; DB 13; Length 864;
Best Local Similarity 96.3%; Pred. No. 1.2e-171;
Matches 830; Conservative 0; Mismatches 24; Indels 8; Gaps 4;

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Qy       1596 TTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGAC 1655
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Db          1 TTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGAC 60

Qy       1656 TTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTT 1715
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTT 120

Qy       1716 TGTGGCACTGAATGGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCGAC 1775
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGTGGCACTGAATGGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCGAC 180

Qy       1776 GGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTC 1835
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTC 240

Qy       1836 ACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGG 1895
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGG 300

Qy       1896 AGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGC 1955
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGC 360

Qy       1956 CATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTG 2015
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Db        361 CATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTG 420

Qy       2016 CGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCAC 2075
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Db        421 CGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCAC 480

Qy       2076 CCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACAC 2135
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Db        481 CCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACAC 540

Qy       2136 TCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCT 2195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCT 600

Qy       2196 CGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGACCT 2255
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Db        601 CGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGACCT 660

Qy       2256 GACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCG 2315
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Qy       2316 CGGCAGCCGCG-AGTGGGAGAGGAACCA-GAACCTCATCAATGCCTGCACAAAGGACATG 2373
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Db        721 CGGCAACCGCGAAGTGGGAGAAGAACCANNAACCTCATCAATGCCTGCACAAAGGACATG 780

Qy       2374 CCCCCCATGGG--CTCCCCTGTGATTCCCACGGACCTG----CCCCTGCGGGCCTCCCCC 2427
              ||||||||||    |||   ||||| ||||||||| |    ||     ||||||||||
Db        781 CCCCCCATGGGGCTCCCCTGNTGATTTCCACGGACCCGTGCCCCTGNCGGGGCCTCCCCC 840

Qy       2428 AGCCACATCCCCAGCGTGGTGG 2449
              |||   ||| ||  |  || ||
Db        841 AGCACAATCNCCCCCAAGGGGG 862


RESULT 14
BU838082
LOCUS       BU838082                 874 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_8071571 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6088226
            5', mRNA sequence.
ACCESSION   BU838082
VERSION     BU838082.1  GI:24022477
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2326  row: b  column: 03
            High quality sequence stop: 652.
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                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
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NIH_MGC Library."

ORIGIN

Query Match 24.8%; Score 767.4; DB 13; Length 874;
Best Local Similarity 99.2%; Pred. No. 4.8e-171;
Matches 771; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       1286 CTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 1345
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Db          1 CTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 60

Qy       1346 AGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA 1405
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Db         61 AGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA 120

Qy       1406 TGAGTGTTTACAACTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG 1465
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGAGTGTTTACAACTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG 180

Qy       1466 GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA 1525
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Db        181 GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA 240

Qy       1526 AGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAAAAAAAACCTGTATTGCCTCCA 1585
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Db        241 AGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAAAAAAAACCTGTATTGCCTCCA 300

Qy       1586 GAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACA 1645
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Qy       1646 GCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTC 1705
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Db        361 GCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTC 420

Qy       1706 ACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACAT 1765
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Qy       1766 CAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATC 1825
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Qy       1826 TGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAG 1885
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Db        541 TGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAG 600

Qy       1886 ACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCA 1945
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Db        601 ACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCA 660

Qy       1946 CCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCA 2005
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Qy       2006 CCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGG 2062
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Db        721 CCGTCTACTGCGTCTGTGATCATCGGCGCCAAGACGTGGCTGTGGTGCCACGCCAAG 777


RESULT 15
BQ683009
LOCUS       BQ683009                 890 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8208014 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6262587
            5', mRNA sequence.
ACCESSION   BQ683009
VERSION     BQ683009.1  GI:21795688
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 890)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2425  row: c  column: 04
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                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             24.6%;  Score 760.6;  DB 13;  Length 890;
  Best Local Similarity   97.0%;  Pred. No. 2e-169;
  Matches  808;  Conservative    0;  Mismatches   19;  Indels    6;  Gaps    3;

Qy       1286 CTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGA 1345
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Qy       1346 AGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA 1405
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Db         61 AGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGA 120

Qy       1406 TGAGTGTTTACAACTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG 1465
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Db         121 TGAGTGTTTACAACTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGG 180

Qy       1466 GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA 1525
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Db         181 GCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAA 240

Qy       1526 AGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCA 1585
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Qy       1826 TGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAG 1885
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Qy       1886 ACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCA 1945
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Qy       1946 CCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCA 2005
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Qy       2006 CCGTCTACTGCGTCTGTGATCATCGGCGCAAAG-ACGTGGCTGTGGTGCAGCGCAAGG-- 2062
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Qy       2063 --AGAAGGAGCTCACCCACTCGCGCCGGGGCTCCA-TGAGCAGCGTCACCAAG 2112
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Search completed: March 26, 2004, 06:35:37
Job time : 8396.21 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 21:56:51 ; Search time 12300 Seconds
(without alignments)
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Title: US-09-856-681A-1
Perfect score: 3093
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3093	100.0	3093	6	AX026741	AX026741 Sequence
2	3093	100.0	3862	6	AX026746	AX026746 Sequence
3	3093	100.0	3862	9	AF279656	AF279656 Homo sapi
4	3038	98.2	3498	6	BD274938	BD274938 POLYNUCLE
5	3032	98.0	4250	9	AB037789	AB037789 Homo sapi
6	2975	96.2	4982	6	AX780545	AX780545 Sequence
7	2969.6	96.0	6060	6	AX884099	AX884099 Sequence
8	2969.6	96.0	6060	6	BD160721	BD160721 Primer fo
9	2969.6	96.0	6060	9	AK027867	AK027867 Homo sapi
10	2746.2	88.8	3550	6	AX099520	AX099520 Sequence
11	2746.2	88.8	3550	6	BD190797	BD190797 Secreted
12	2698	87.2	3333	6	BD274939	BD274939 POLYNUCLE
13	2584	83.5	4702	10	BC059238	BC059238 Mus muscu
14	2414.8	78.1	3018	10	AF288666	AF288666 Mus muscu
15	2282.4	73.8	4139	10	BC062979	BC062979 Mus muscu
16	2182.4	70.6	3041	6	AX882248	AX882248 Sequence
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23	1824.4	59.0	2293	9	AK027471	AK027471 Homo sapi
24	1742.4	56.3	2227	6	BD127394	BD127394 Primer fo
25	1742.4	56.3	2227	9	AK074975	AK074975 Homo sapi
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33	1200	38.8	131823	2	AC010497	AC010497 Homo sapi

c	34	1200	38.8	134349	9	AC010296	AC010296 Homo sapi
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	36	1200	38.8	179647	2	AC108124	AC108124 Homo sapi
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	39	1023.8	33.1	169529	10	AC124466	AC124466 Mus muscu
c	40	1023.8	33.1	170386	2	AC124181	AC124181 Mus muscu
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ALIGNMENTS

RESULT 1
AX026741
LOCUS AX026741 3093 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 1 from Patent WO0031252.
ACCESSION AX026741
VERSION AX026741.1 GI:10187886
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Klostermann,A. and Behl,C.
TITLE Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal development and regeneration mechanisms during apoptosis, and its use as a potential drug target
JOURNAL Patent: WO 0031252-A 1 02-JUN-2000;
KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL CHRISTIAN (DE)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 3093; DB 6; Length 3093;
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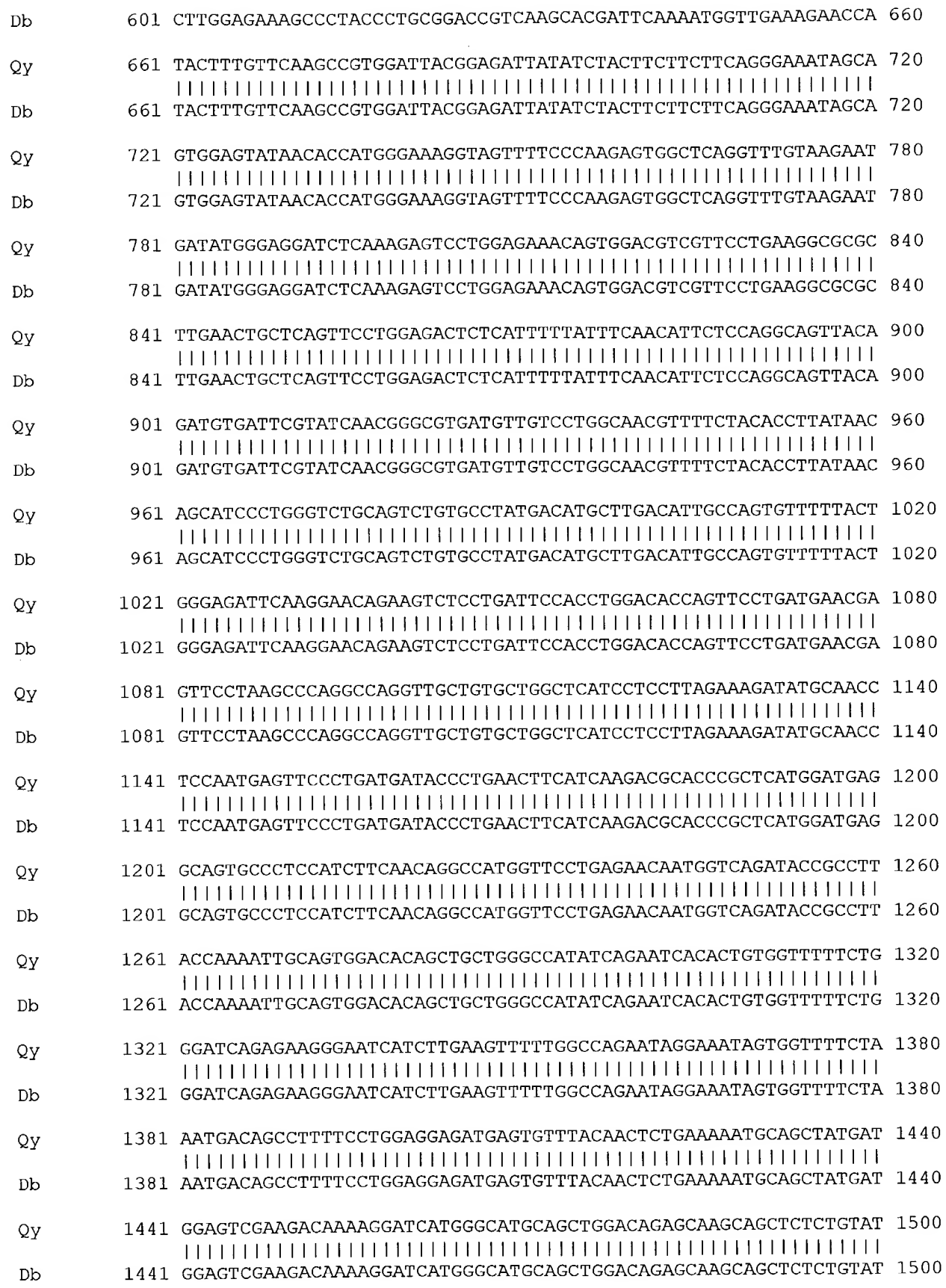
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DEFINITION Sequence 6 from Patent WO0031252.

ACCESSION AX026746
VERSION AX026746.1 GI:10187890
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Klostermann,A. and Behl,C.
TITLE Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal development and regeneration mechanisms during apoptosis, and its use as a potential drug target
JOURNAL Patent: WO 0031252-A 6 02-JUN-2000;
KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL CHRISTIAN (DE)
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ORIGIN

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Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
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RESULT 3
AF279656
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DEFINITION  Homo sapiens semaphorin SEMA6A1 mRNA, complete cds.
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VERSION     AF279656.1  GI:11093650
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SOURCE      Homo sapiens (human)
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REFERENCE   1  (bases 1 to 3862)
  AUTHORS   Klostermann,A., Lutz,B., Gertler,F. and Behl,C.
  TITLE     The orthologous human and murine semaphorin 6A-1 proteins
            (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated
            phosphoprotein-like protein (EVL) via a novel carboxyl-terminal
            zyxin-like domain
  JOURNAL   J. Biol. Chem. 275 (50), 39647-39653 (2000)
  MEDLINE   20564339
   PUBMED   10993894
REFERENCE   2  (bases 1 to 3862)
  AUTHORS   Klostermann,A., Lutz,B., Gertler,F. and Behl,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUN-2000) Independent Research Group
            Neurodegeneration, MPI of Psychiatry, Kraepelinstrasse 2-10, Munich
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80804, Germany

FEATURES Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 3093; DB 9; Length 3862;
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Db       2038 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 2097

Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
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Db       2098 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 2157

Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1561 TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
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Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
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Qy       1681 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1740
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Qy       1741 TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG 1800
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Qy       2101 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2160
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Db       2758 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2817

Qy       2161 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2220
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Qy       2521 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2580
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Qy       2581 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2640
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Db       3238 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 3297

Qy       2641 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
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Qy       2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC 2820
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Qy       3001 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3060
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Db       3658 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3717

Qy       3061 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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Db       3718 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3750


RESULT 4
BD274938
LOCUS       BD274938                3498 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY.
ACCESSION   BD274938
VERSION     BD274938.1  GI:33084706
KEYWORDS    JP 2002538786-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3498)
  AUTHORS   Shimkets,R.A.
  TITLE     POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
  JOURNAL   Patent: JP 2002538786-A 2 19-NOV-2002;
            CuraGen Corporation,Richard A Shimkets
COMMENT     OS   Homo sapiens
            PN   JP 2002538786-A/2
            PD   19-NOV-2002
            PF   09-MAR-2000 JP 2000603363
            PR   08-MAR-2000 US    09/520781,09-MAR-1999 US    60/123667 PI
            richard a shimkets
            CC
            FH   Key             Location/Qualifiers
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            FT   misc_feature    (3047)
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            FT                   c'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.2%;  Score 3038;  DB 6;  Length 3498;
  Best Local Similarity   99.3%;  Pred. No. 0;
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Matches 3072; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db        214 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 273

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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Db        274 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db        334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
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Db        454 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 513

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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Db        514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 573

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
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Db        574 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 633

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Db        634 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 693

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
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Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
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Db        814 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 873

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
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Db        874 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 933

Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
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Db        934 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 993

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Qy        841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
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Db       1054 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1113

Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
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Db       1114 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1173

Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
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Db       1174 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1233

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
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Db       1234 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1293

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
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Db       1294 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1353

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
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Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
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Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
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Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
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Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
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Qy       1681 AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1740
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Qy       1921 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 1980
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Qy       2281 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC 2340
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Qy       2401 ACGGACCTGCCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2460
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Qy       2461 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2520
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Qy       2641 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
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Qy       2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
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Db       2914 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2973

Qy       2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAAGAAACAACACTAA 2819
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Db       2974 CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA 3033

Qy       2820 CTCCTCCAATTCCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC 2878
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Qy       2879 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 2938
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Db       3094 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 3153

Qy       2939 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 2998
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Qy       2999 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3058
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Qy       3059 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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DEFINITION  Homo sapiens mRNA for KIAA1368 protein, partial cds.
ACCESSION   AB037789
VERSION     AB037789.1  GI:7243116
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (sites)
  AUTHORS   Nagase,T., Kikuno,R., Ishikawa,K.I., Hirosawa,M. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XVI. The complete sequences of 150 new cDNA clones from brain which
            code for large proteins in vitro
  JOURNAL   DNA Res. 7 (1), 65-73 (2000)
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  MEDLINE   20181126
   PUBMED   10718198
REFERENCE   2  (bases 1 to 4250)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
            Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
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                     LKEPYFVQAVDYGDYIYFFFREIAVEYNTMGKVVFPRVAQVCKNDMGGSQRVLEKQWT
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ORIGIN

  Query Match             98.0%;  Score 3032;  DB 9;  Length 4250;
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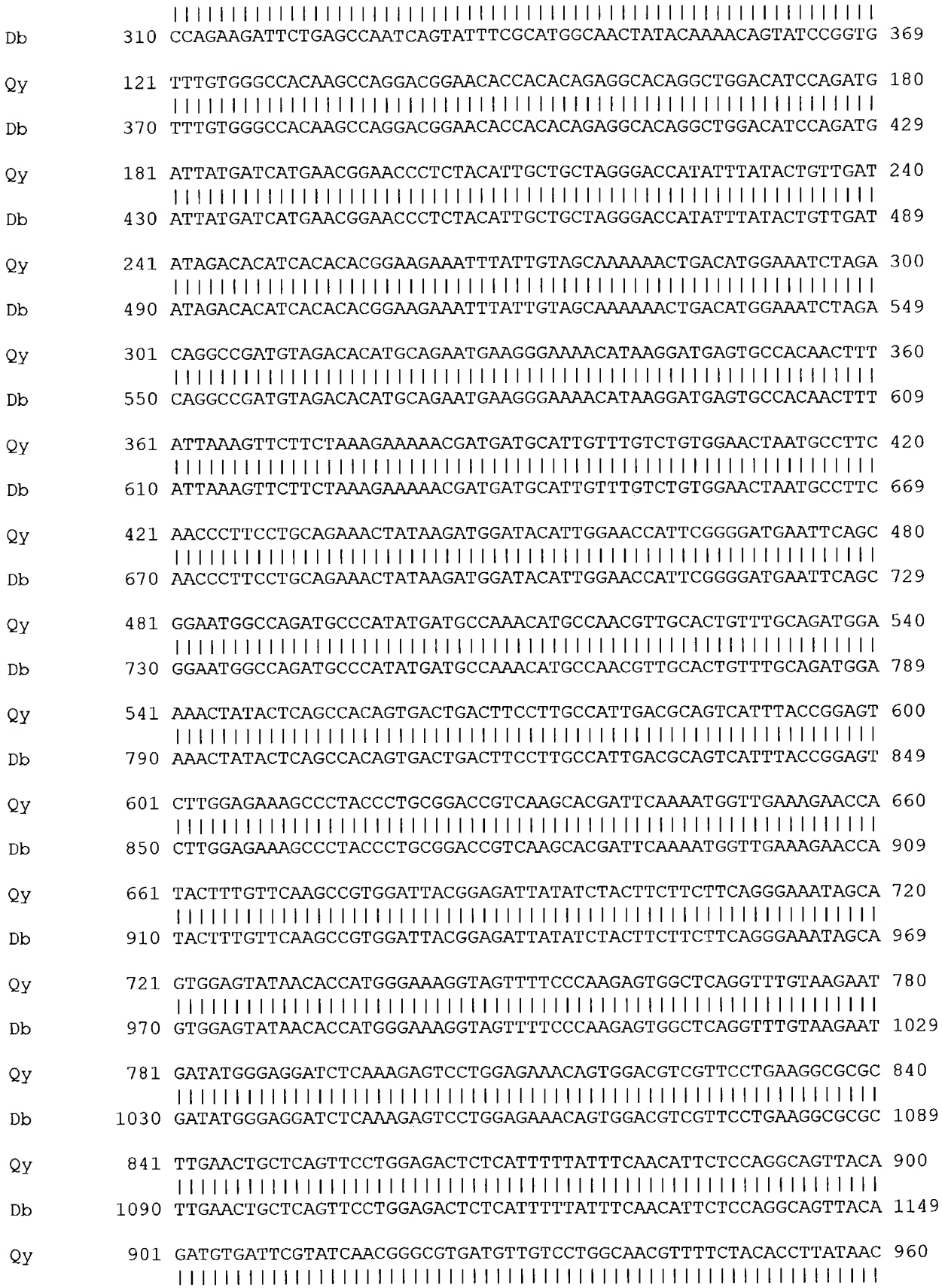

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1269

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
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Db       1270 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1329

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
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Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
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Db       1390 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1449

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
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Db       1450 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1509

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
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Db       1510 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1569

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
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Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Db       1630 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1689

Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
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Db       1690 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1749

Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
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Qy       1561 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
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Db       1870 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1929

Qy       1681 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGA---------------- 1726
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Db       1930 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT 1989

Qy       1727 ------------------------------------ATGGGCATTCCAGTTCCCTCTTG 1749
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Qy       1750 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 1809
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Db       2050 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 2109

Qy       1810 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT 1869
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Qy       1870 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGAC 1929
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Qy       1930 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC 1989
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Qy       1990 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 2049
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Qy       2290 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC 2349
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Qy       2350 ATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 2409
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RESULT 6
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DEFINITION  Sequence 2702 from Patent WO03039443.
ACCESSION   AX780545
VERSION     AX780545.1  GI:32697539
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
            Dugas,M., Eils,R., Brors,B. and Mergenthaler,S.
  TITLE     Novel genetic markers for leukemias
  JOURNAL   Patent: WO 03039443-A 2702 15-MAY-2003;
            Deutsches Krebsforschungszentrum (DE) ;
            Ludwig-Maximilian-Universitaet Muenchen (DE) ; Haferlach, Torsten,
            PD Dr. Dr. (DE) ; Schoch, Claudia (DE) ; Kern, Wolfgang (DE)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             96.2%;  Score 2975;  DB 6;  Length 4982;
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Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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Db        672 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 731

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db        732 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 791

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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Db        792 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 851

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
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Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
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Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Qy        780 TGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCG 839
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Qy        840 CTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTAC 899
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Qy       1200 GGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCT 1259
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Qy       1260 TACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCT 1319
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RESULT 7
AX884099
LOCUS AX884099 6060 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 19004 from Patent EP1074617.
ACCESSION AX884099

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VERSION     AX884099.1  GI:40039000
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primers for synthesising full-length cDNA and their use
  JOURNAL   Patent: EP 1074617-A 19004 07-FEB-2001;
            Research Association for Biotechnology (JP)
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ORIGIN

  Query Match             96.0%;  Score 2969.6;  DB 6;  Length 6060;
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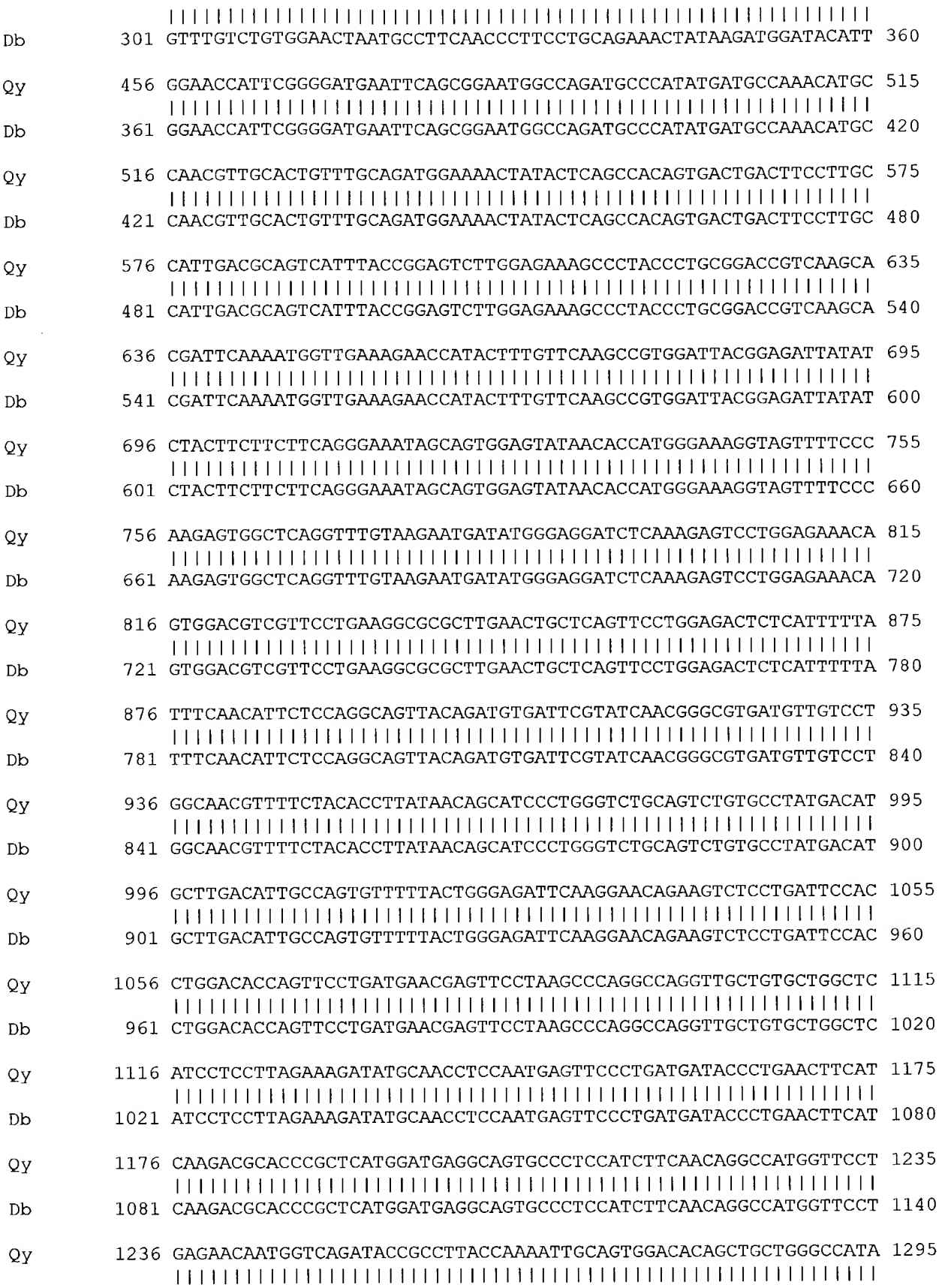

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Qy       2734 TACGGGGTTGACTATAAGAGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGCC 2793
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Qy       2974 TACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCC 3033
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Qy       3034 CCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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RESULT 8
BD160721
LOCUS       BD160721                6060 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD160721
VERSION     BD160721.1  GI:27866479
KEYWORDS    JP 2002191363-A/15564.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6060)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 15564 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
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            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
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            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC
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            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
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ORIGIN

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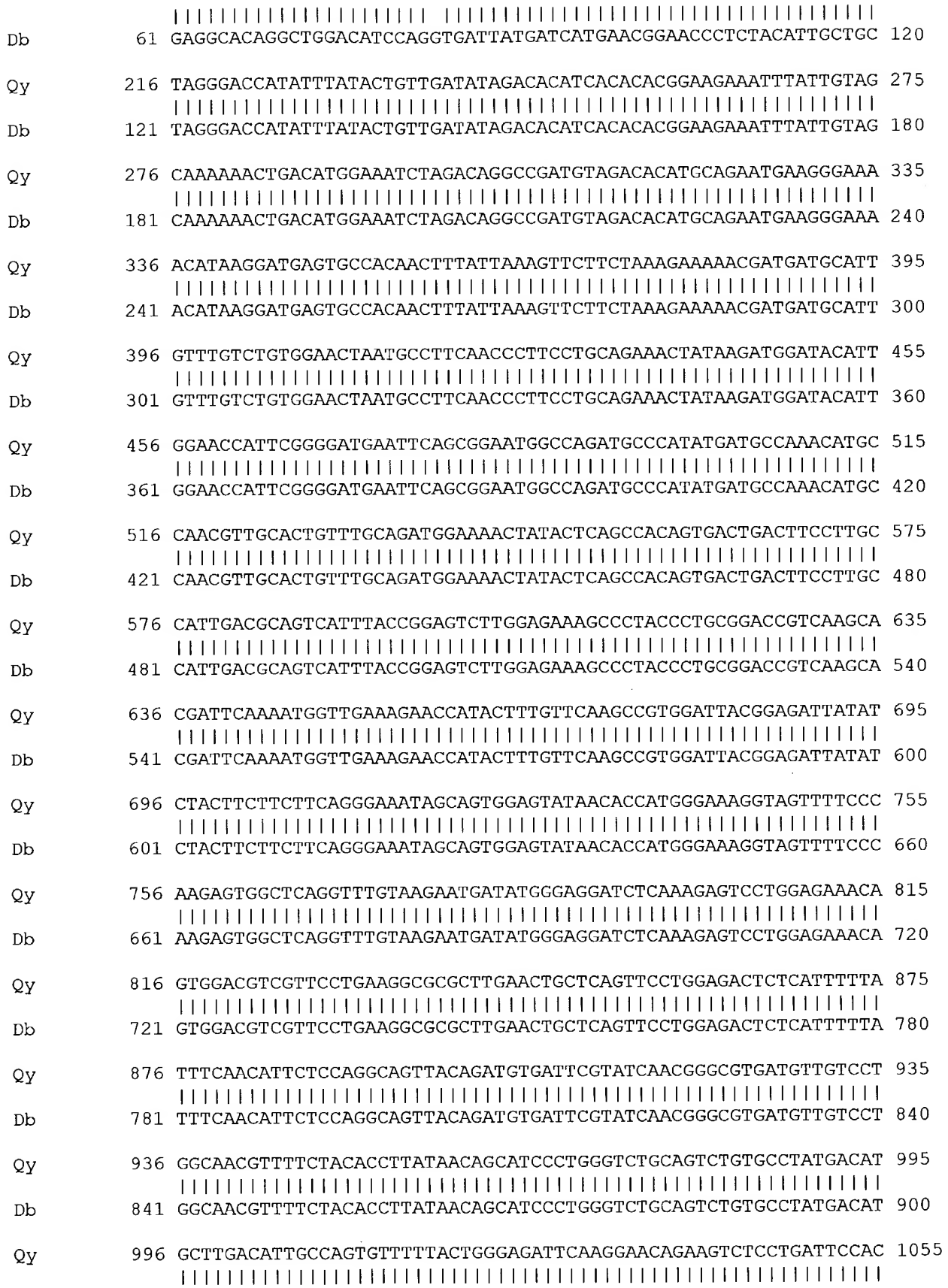
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Qy 816 GTGGACGTCGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTA 875
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Qy       1236 GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA 1295
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Db       1141 GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA 1200

Qy       1296 TCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGC 1355
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Qy       1356 CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA 1415
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Db       1261 CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA 1320

Qy       1416 CAACTCTG-AAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGC 1474
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Qy       1894 GGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG 1953
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RESULT 9
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DEFINITION  Homo sapiens cDNA FLJ14961 fis, clone PLACE4000230, highly similar
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ACCESSION   AK027867
VERSION     AK027867.1  GI:14042853
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
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  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 6060)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction,
            5'- & 3'-end one pass sequencing and clone selection: Helix
            Research Institute (supported by Japan Key Technology Center etc.)
            and Department of Virology, Institute of Medical Science,
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University of Tokyo.

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ORIGIN
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Query Match 96.0%; Score 2969.6; DB 9; Length 6060;
Best Local Similarity 99.8%; Pred. No. 0;
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Qy        516 CAACGTTGCACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGC 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAACGTTGCACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGC 480

Qy        576 CATTGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCA 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CATTGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCA 540

Qy        636 CGATTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        696 CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCC 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCC 660

Qy        756 AAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACA 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACA 720

Qy        816 GTGGACGTCGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTA 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGGACGTCGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTA 780

Qy        876 TTTCAACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCT 935
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Db        781 TTTCAACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCT 840

Qy        936 GGCAACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACAT 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        996 GCTTGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC 1055
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Db        901 GCTTGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC 960

Qy       1056 CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC 1115
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Db        961 CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC 1020

Qy       1116 ATCCTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCAT 1175
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Db       1021 ATCCTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCAT 1080

Qy       1176 CAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCT 1235
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCT 1140

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Db       1141 GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA 1200

Qy       1296 TCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGC 1355
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Db       1201 TCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGC 1260

Qy       1356 CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA 1415
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Db       2161 CTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC 2220

Qy       2314 CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG 2373
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Db       2221 CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG 2280

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Db       2281 CCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCAC 2340

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Qy       2554 TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG 2613
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Db       2461 TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG 2520

Qy       2614 GAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCG 2673
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Db       2521 GAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCG 2580

Qy       2674 GGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCC 2733
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Qy       2734 TACGGGGTTGACTATAAGAGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGCC 2793
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Qy       2794 ACCACTCTCAAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAG 2853
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Db       2701 ACCACTCTCAAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAG 2760

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Db       2761 AGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCCGCAGAGGGTGGACTCCATCCAGGTG 2820

Qy       2914 CACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCC 2973
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Db       2821 CACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCC 2880

Qy       2974 TACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCC 3033
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Db       2881 TACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCC 2940

Qy       3034 CCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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RESULT 10
AX099520
LOCUS       AX099520               3550 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 160 from Patent WO0119988.
ACCESSION   AX099520
VERSION     AX099520.1  GI:13538594
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Collins-Racie,L.A., Evans,C.,
            Merberg,D., Treacy,M., Bowman,M.R., Spaulding,V. and Agostino,M.J.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: WO 0119988-A 160 22-MAR-2001;
            Genetics Institute, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .3550
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ORIGIN

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  Best Local Similarity   94.5%;  Pred. No. 0;
  Matches 2923;  Conservative    1;  Mismatches    4;  Indels  165;  Gaps    1;

Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 185

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 245

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 305

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 365

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              |||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        366 ATAGACACATCACACACSGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 425

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 485

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 545
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Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 605

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 665

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Db        666 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 725

Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
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Db        726 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 785

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
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Db        786 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 845

Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
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Db        846 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 905

Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
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Db        906 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 965

Qy        841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1025

Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
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Db       1026 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1085

Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1145

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
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Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
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Db       1206 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1265

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
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Db       1266 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1325

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1385
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Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
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Db       1386 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1445

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Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Db       1506 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1565

Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
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Db       1566 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1625

Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
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Db       1626 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1685

Qy       1561 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
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Db       1686 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1745

Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
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Db       1746 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1805

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Qy       1741 TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG 1800

Db       1854 ------------------------------------------------------------ 1853

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Db       1854 ------------------------------------------------------------ 1853

Qy       1861 GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA 1920
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Qy       1921 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 1980
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Db       1881 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 1940

Qy       1981 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC 2040
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Qy       2041 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC 2100
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Db       2001 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC 2060

Qy       2101 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2160
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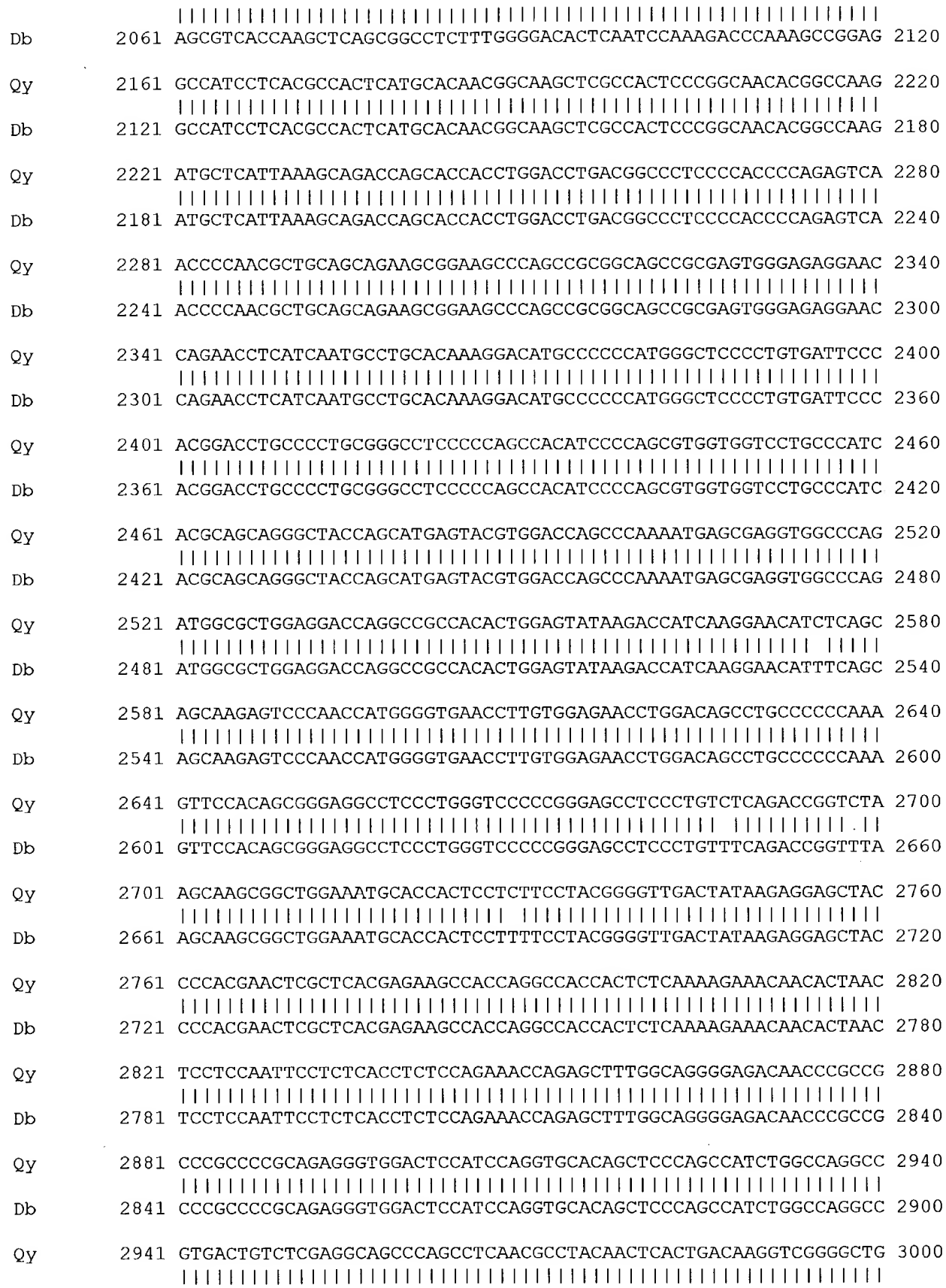

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Db       2961 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3020

Qy       3061 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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RESULT 11
BD190797
LOCUS       BD190797               3550 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Secreted proteins and polynucleotides encoding them.
ACCESSION   BD190797
VERSION     BD190797.1  GI:33000536
KEYWORDS    JP 2002514063-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 3550)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: JP 2002514063-A 5 14-MAY-2002;
            GENETICS INSTITUTE INC Louis O Gerrue,Jonathan M Diver
COMMENT     PN   JP 2002514063-A/5
            PD   14-MAY-2002
            PF   17-DEC-1997 JP 1998527963
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ORIGIN

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Db        126 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 185

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 245
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Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db        246 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 305

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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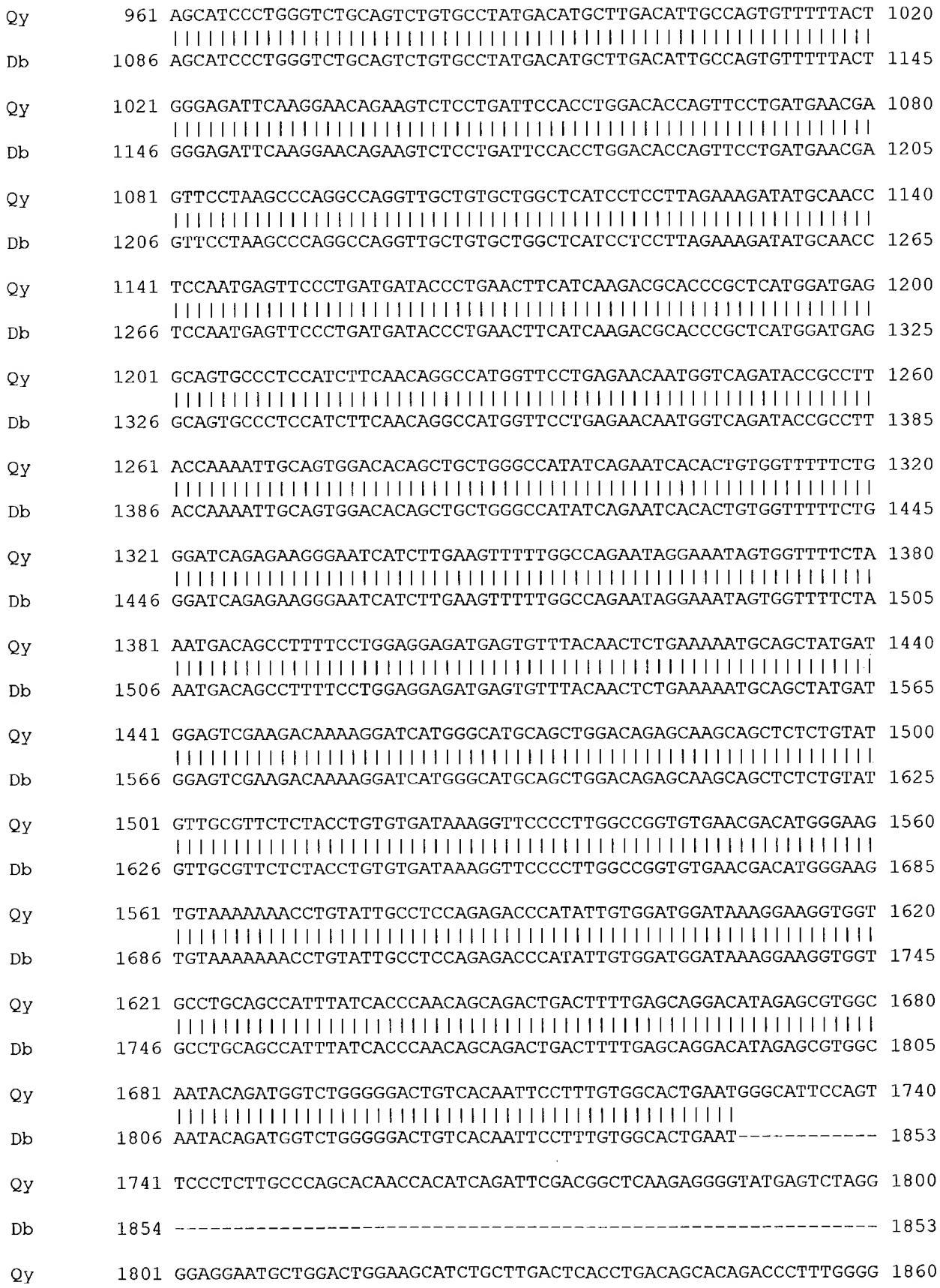
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DEFINITION  POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY.
ACCESSION   BD274939
VERSION     BD274939.1  GI:33084707
KEYWORDS    JP 2002538786-A/3.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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  AUTHORS   Shimkets,R.A.
  TITLE     POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
  JOURNAL   Patent: JP 2002538786-A 3 19-NOV-2002;
            CuraGen Corporation,Richard A Shimkets
COMMENT     OS   Homo sapiens
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            PD   19-NOV-2002
            PF   09-MAR-2000 JP 2000603363
            PR   08-MAR-2000 US    09/520781,09-MAR-1999 US    60/123667 PI
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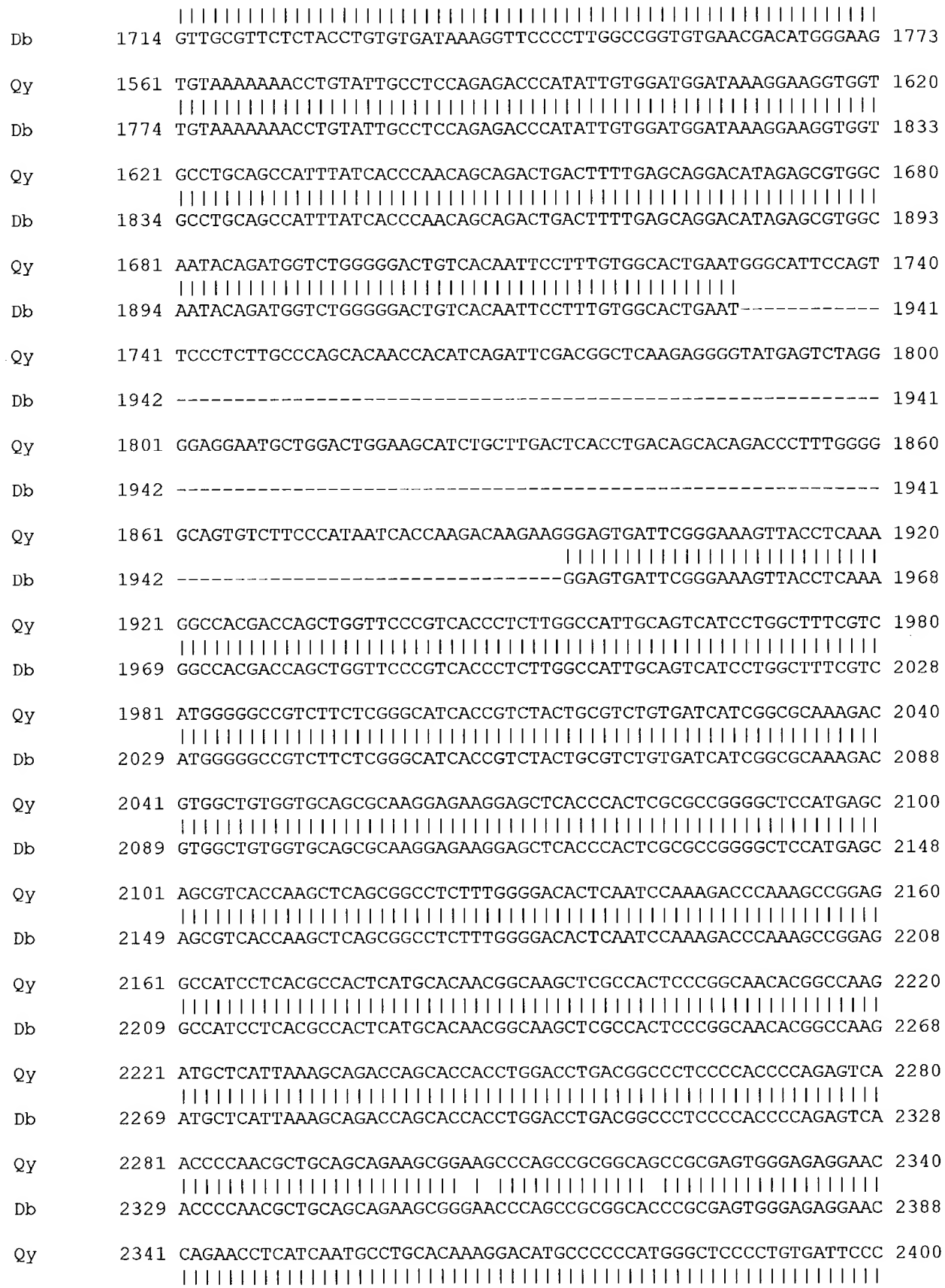

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RESULT 13
BC059238
LOCUS BC059238 4702 bp mRNA linear ROD 20-OCT-2003
DEFINITION Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A, mRNA (cDNA clone MGC:66957 IMAGE:6417475), complete cds.

ACCESSION BC059238
VERSION BC059238.1 GI:37748386
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4702)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 4702)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 125 Row: o Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9055333.
FEATURES Location/Qualifiers

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ORIGIN

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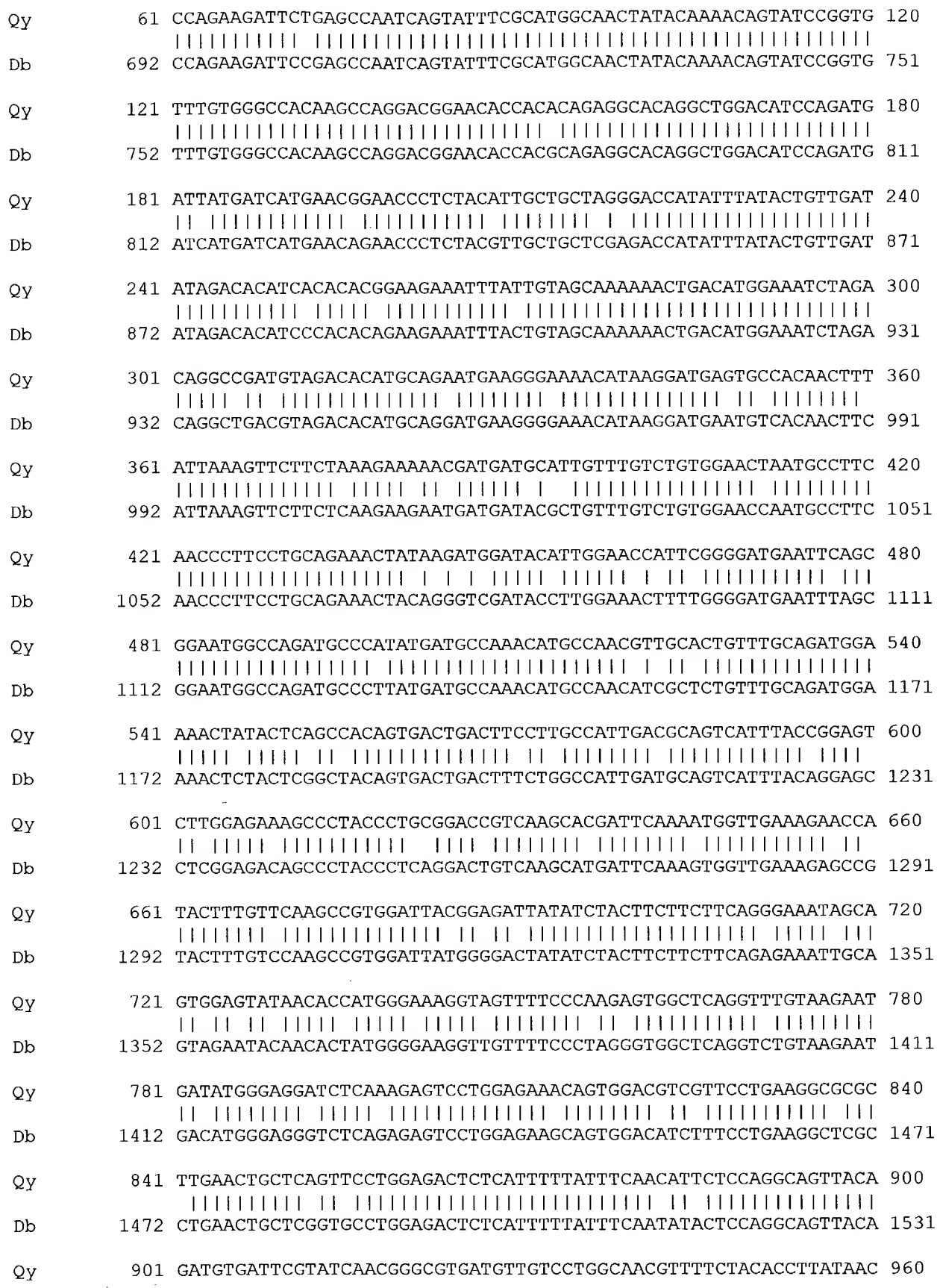

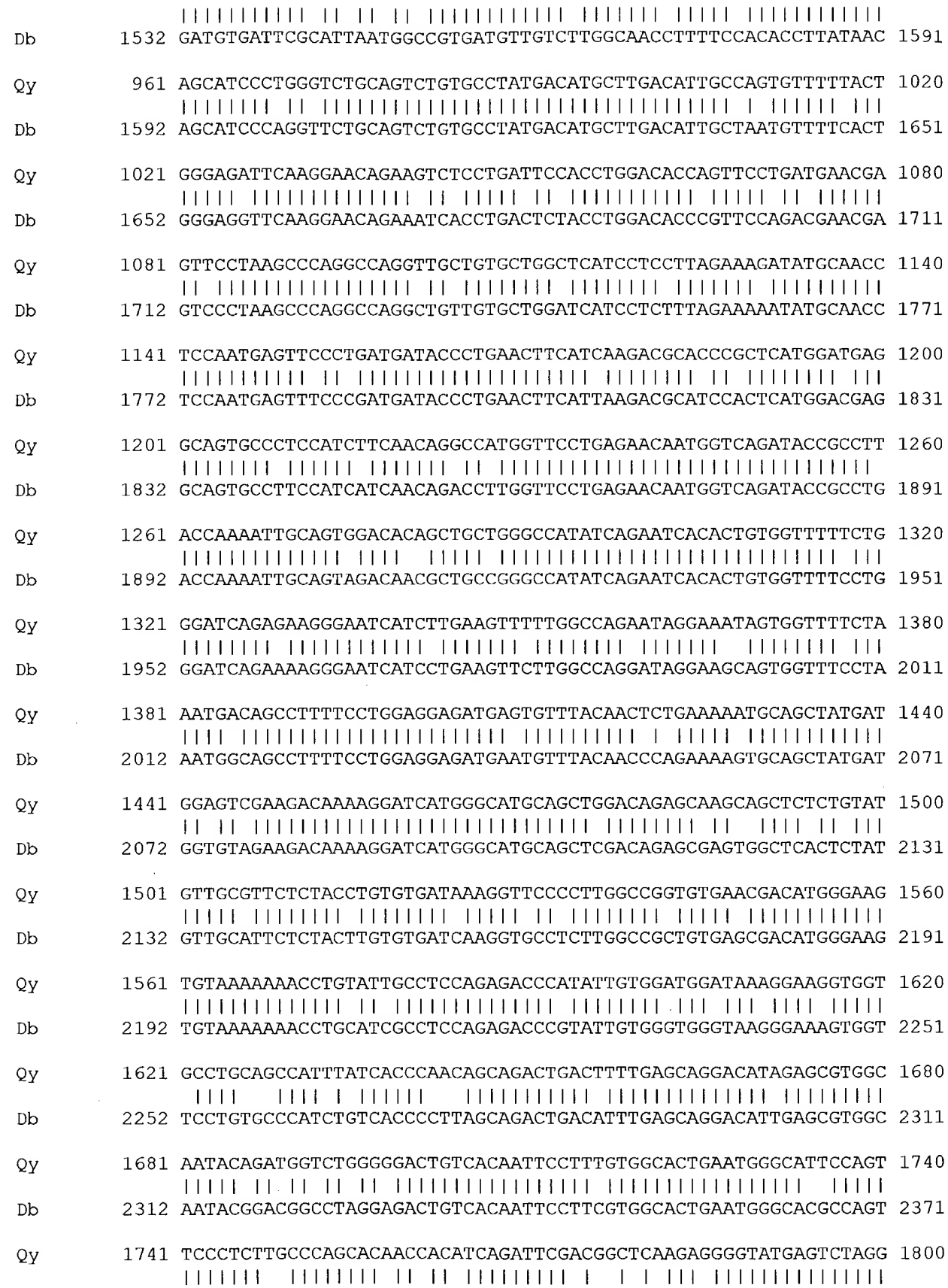

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SOURCE      Mus musculus (house mouse)
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REFERENCE   1  (bases 1 to 3018)
  AUTHORS   Klostermann,A., Lutz,B., Gertler,F. and Behl,C.
  TITLE     The orthologous human and murine semaphorin 6A-1 proteins
            (SEMA6A-1/Sema6A-1) bind to the enabled/vasodilator-stimulated
            phosphoprotein-like protein (EVL) via a novel carboxyl-terminal
            zyxin-like domain
  JOURNAL   J. Biol. Chem. 275 (50), 39647-39653 (2000)
  MEDLINE   20564339
   PUBMED   10993894
REFERENCE   2  (bases 1 to 3018)
  AUTHORS   Klostermann,A. and Behl,C.
  TITLE     Direct Submission
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  JOURNAL   Submitted (21-JUL-2000) Independent Research Group
            Neurodegeneration, MPI of Psychiatry, Kraepelinstrasse 2-10, Munich
            80804, Germany
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ORIGIN

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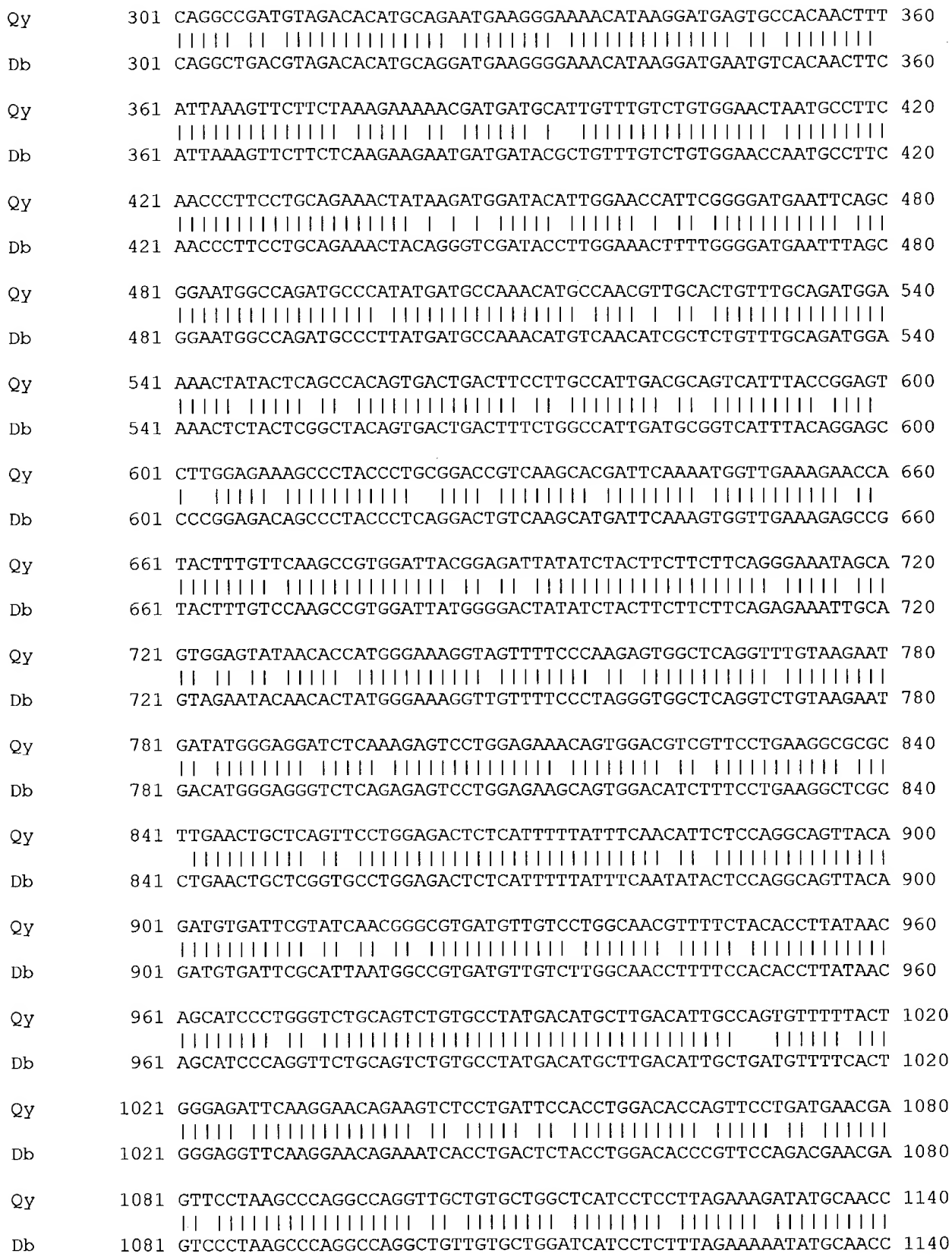

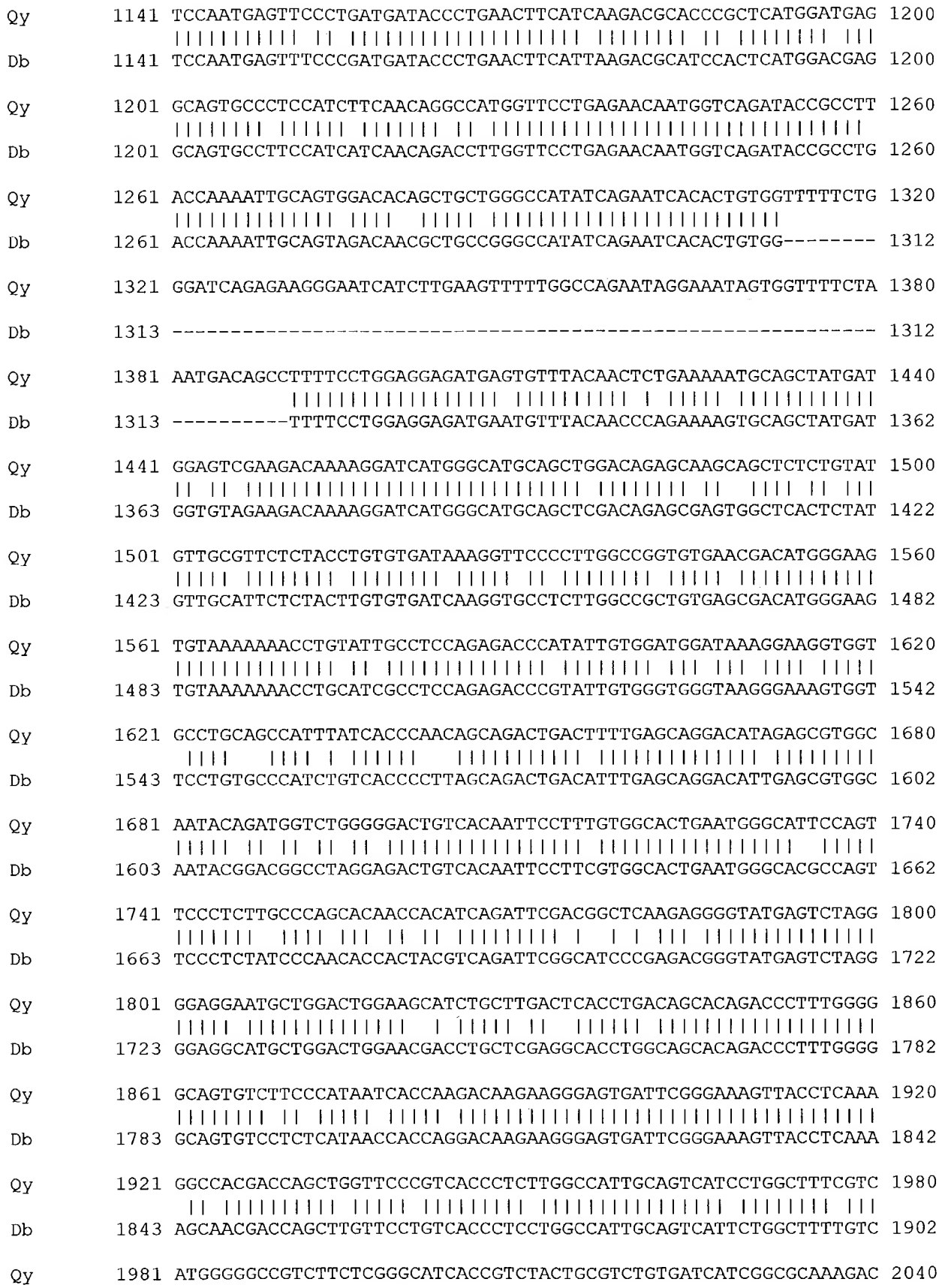

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DEFINITION  Mus musculus sema domain, transmembrane domain (TM), and
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ACCESSION   BC062979
VERSION     BC062979.1  GI:38566245
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SOURCE      Mus musculus (house mouse)
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 4139)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
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            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 4139)
  AUTHORS   Strausberg,R.
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TITLE Direct Submission
JOURNAL Submitted (26-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A., Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K., Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J., Casavant,T., Soares,M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: Plate: Row: Column: 0.

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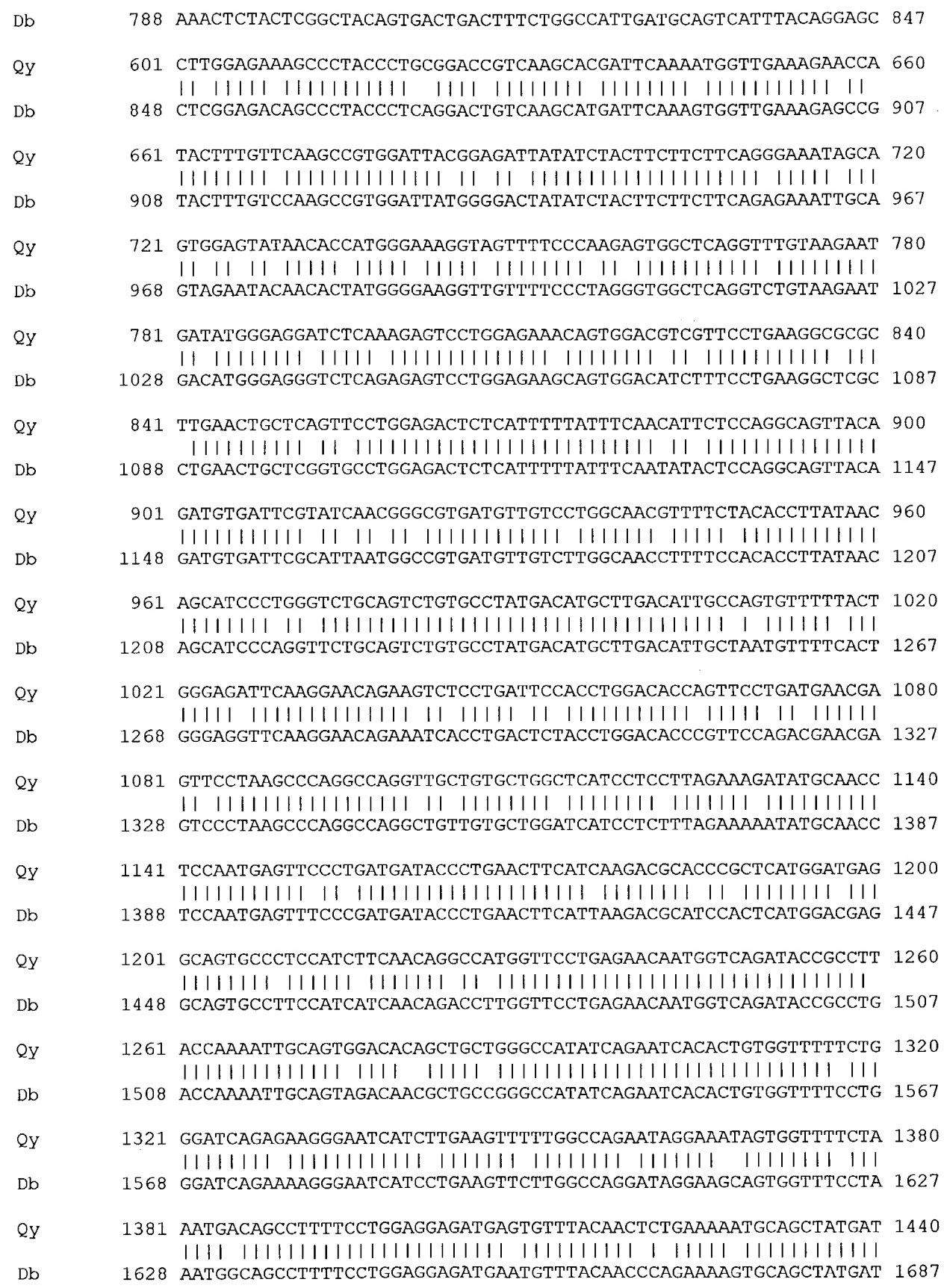

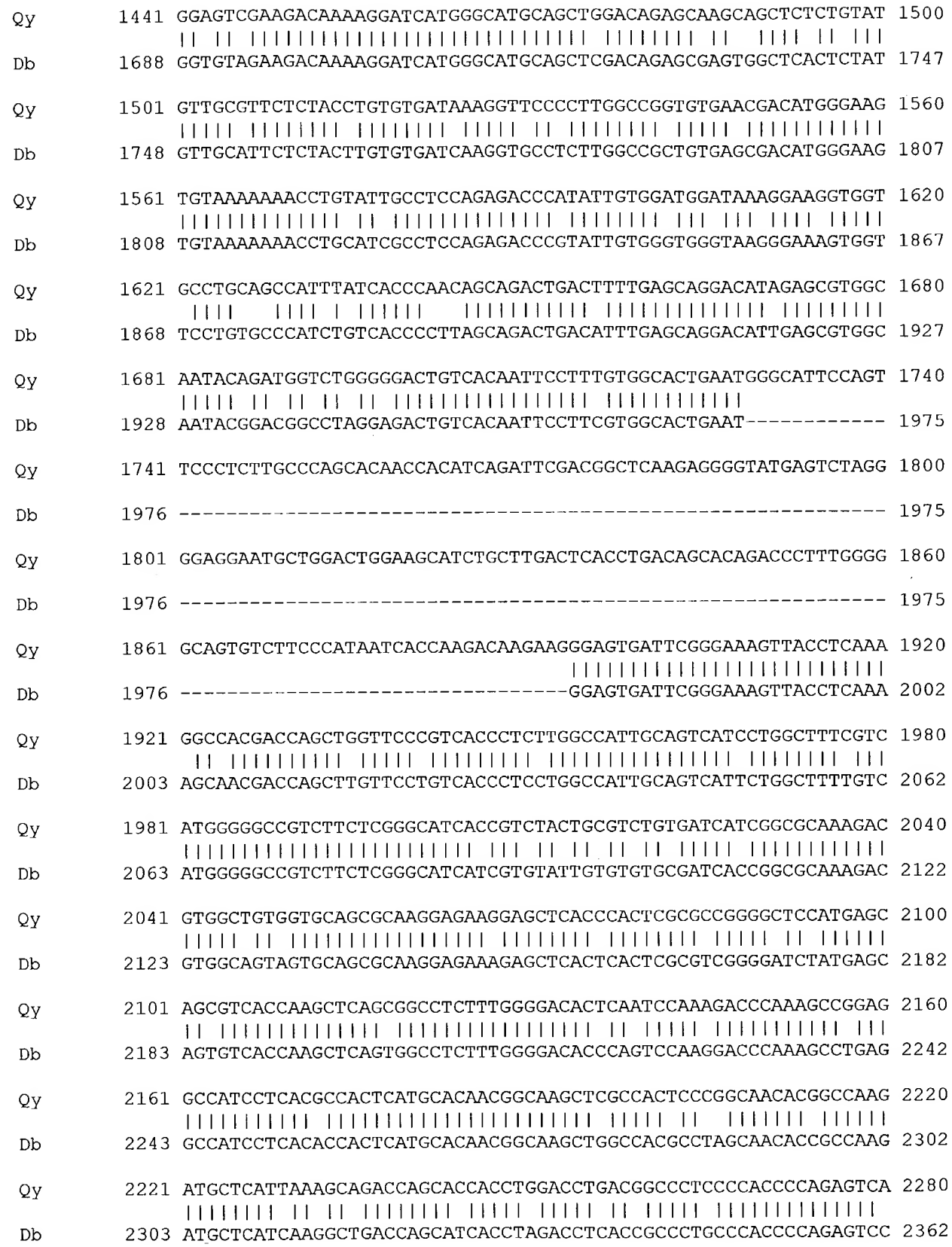

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	2969.6	96.0	6060	4	AAH18729	Aah18729 Human cDN
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8	2746.2	88.8	3550	5	AAF98469	Aaf98469 Human cDN
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ALIGNMENTS

RESULT 1
AAD01233
ID AAD01233 standard; DNA; 3862 BP.
XX
AC AAD01233;
XX
DT 04-OCT-2000 (first entry)
XX
DE Human semaphorin 6A-1 cDNA.
XX
KW Human; semaphorin 6A-1; (HSA)SEMA6A-1; neuronal development; apoptosis;
KW neuronal regeneration; Ena/VASP protein family; immunomodulatory;
KW gene therapy; diagnostic agent; therapeutic agent; differentiation;
KW cytoskeletal stabilisation; plasticity; ds.

XX
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XX
FH Key Location/Qualifiers
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FT which selectively binds to members of Ena/VASP protein
FT family"
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PD 02-JUN-2000.
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PF 26-NOV-1999; 99WO-EP009215.
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PR 26-NOV-1998; 98EP-00122441.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Behl C, Klostermann A;
XX
DR WPI; 2000-400065/34.
DR P-PSDB; AAY71460.
XX
PT Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent,
PT therapeutic agent, for modulating immune system, in gene therapy or for
PT effecting differentiation, cytoskeletal stabilization and/or plasticity.
XX
PS Claim 1; Fig 2; 53pp; English.
XX
CC The present sequence is a cDNA encoding transmembranous human semaphorin
CC 6A-1 ((HSA)SEMA6A-1) which is involved in neuronal development and
CC regeneration mechanisms during apoptosis. Semaphorin is a family of
CC proteins displaying secreted or transmembrane-based repulsive guidance
CC cues critically involved in neuronal development. The present sequence
CC was isolated from human 1-ZAP Express cDNA library which was screened
CC using a PCR fragment amplified from human neuroblastoma cell line SK-N-MC
CC cDNA. The (HSA)SEMA6A-1 protein contains a Zyxin-like domain that
CC selectively binds to members of Ena/VASP protein family especially Evl.
CC Expression of (HSA)SEMA6A-1 is highest in embryonic brain and kidney and
CC moderate in lung. The present sequence is useful as diagnostic and
CC therapeutic agents, for modulating the immune system, in gene therapy,
CC for effecting differentiation, cytoskeletal stabilisation and plasticity
XX
SQ Sequence 3862 BP; 971 A; 1111 C; 967 G; 813 T; 0 U; 0 Other;

Query Match 100.0%; Score 3093; DB 3; Length 3862;
Best Local Similarity 100.0%; Pred. No. 0;
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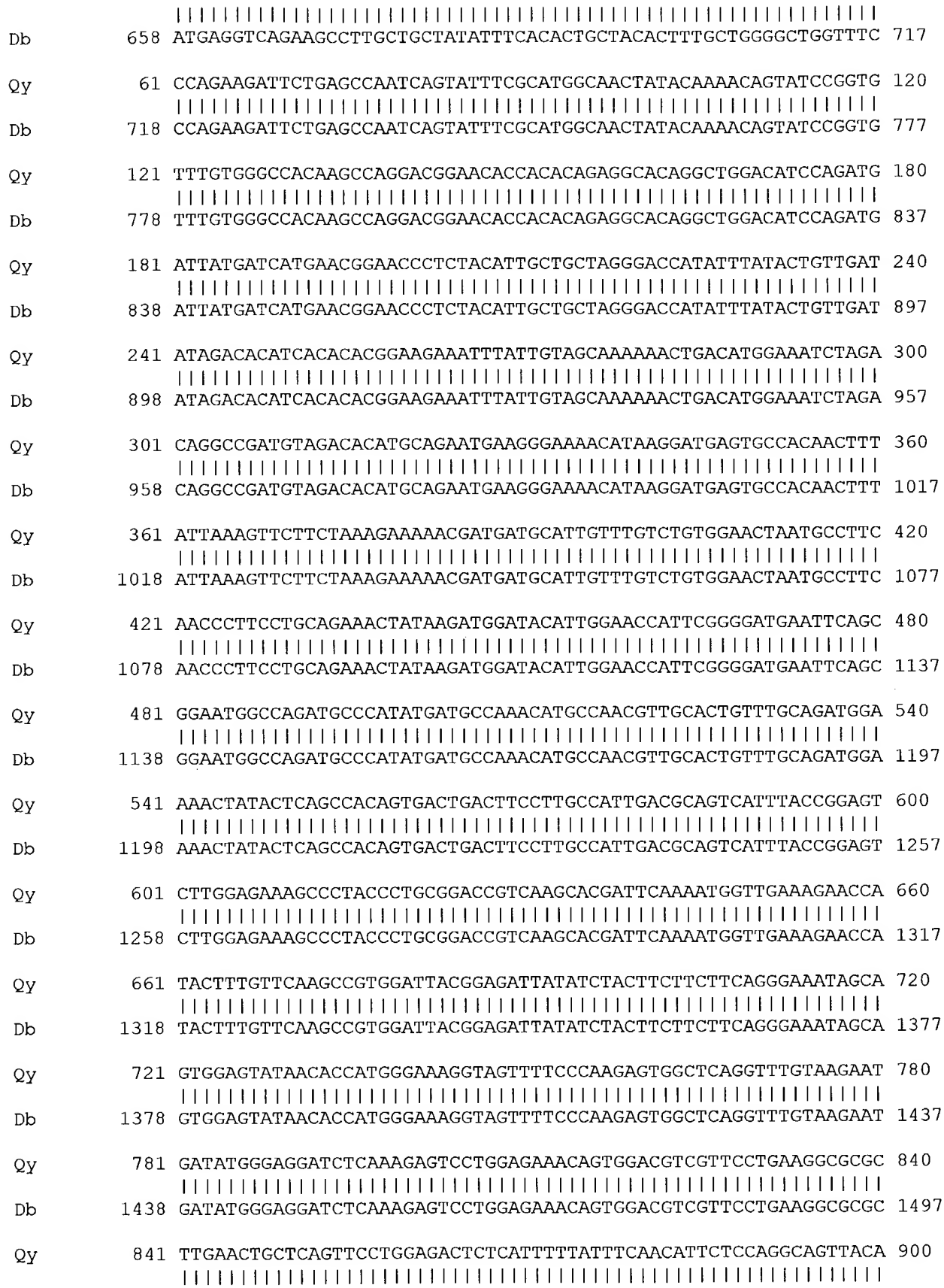
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Qy 61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
Db 718 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 777
Qy 121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
Db 778 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 837
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Qy 241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
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Qy 361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
Db 1018 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 1077
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Db 1138 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 1197
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Db 1198 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 1257
Qy 601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
Db 1258 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 1317
Qy 661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
Db 1318 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 1377
Qy 721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
Db 1378 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 1437
Qy 781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
Db 1438 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1497
Qy 841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900

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Db       1498 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1557

Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1558 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1617

Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1618 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1677

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
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Db       1678 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1737

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1738 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1797

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1798 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1857

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
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Db       1858 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1917

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1918 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1977

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1978 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 2037

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
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Db       2158 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 2217

Qy       1561 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
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Db       2278 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 2337

Qy       1681 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1740
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Qy       1741 TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG 1800
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Qy       1801 GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2458 GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG 2517

Qy       1861 GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA 1920
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Qy       1921 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 1980
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Db       2578 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 2637

Qy       1981 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC 2040
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Qy       2041 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC 2100
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Qy       2101 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2160
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Qy       2161 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2220
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Db       2818 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2877

Qy       2221 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2280
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Qy       2281 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC 2340
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Db       2998 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC 3057

Qy       2401 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2460
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Qy       2521 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2580
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Qy       2581 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2640
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Qy       2641 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
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Qy       2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
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Qy       2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC 2820
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Qy       2821 TCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2881 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 2940
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Qy       2941 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTG 3000
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Qy       3001 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3060
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Db       3658 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3717

Qy       3061 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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Db       3718 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3750
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RESULT 2
AAA93617
ID AAA93617 standard; DNA; 3498 BP.
XX
AC AAA93617;
XX
DT 16-JAN-2001 (first entry)
XX
DE Human semaphorin protein-like splice variant SECX 2864933-1 DNA.
XX
KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy; ds.

XX
OS Homo sapiens.
XX
PN WO200053742-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006280.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 08-MAR-2000; 2000US-0520781P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA;
XX
DR WPI; 2000-594318/56.
DR P-PSDB; AAB23030.
XX
PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.
XX
PS Claim 3; Fig 2; 151pp; English.
XX
CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins of
CC the invention are either secreted or membrane-associated proteins and act
CC as regulator of cellular proliferation and differentiation. SECX proteins
CC or nucleotides are useful for diagnosing the presence of, or
CC predisposition to, a disease associated with altered levels of SECX
CC proteins and nucleotides. The SECX proteins are also useful to screen
CC compounds that modulate SECX activity or expression. The interaction of a
CC SECX protein with other cellular proteins may be useful to modulate the
CC activity of a partner protein, cellular proliferation, cellular
CC differentiation and cell survival. SECX nucleotides are useful for the
CC recombinant expression of SECX protein, and may be used detect SECX mRNA
CC or genetic lesions in the SECX gene. They may also be used to modulate
CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
CC acid sequences are also useful for identifying a cell or tissue type in a
CC biological sample, and in forensic biology. SECX primers or probes are
CC useful for detecting the presence of SECX nucleotides and for screening
CC tissue cultures for contamination. Diseases that may be treated or
CC prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
CC or traumatic wounds, spinal cord injury), and skeletal disorders
XX
SQ Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 0 U; 1 Other;

Query Match 98.2%; Score 3038; DB 3; Length 3498;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3072; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
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Db        214 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 273

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db        334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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Db        394 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 453

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
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Db        454 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 513

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 573

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
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Db        574 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 633

Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
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Db        634 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 693

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 753

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Db        754 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 813

Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
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Db        814 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 873

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 933

Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 993

Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1053
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Qy       841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
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Db      1054 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1113

Qy       901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1173

Qy       961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1233

Qy      1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
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Db      1234 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1293

Qy      1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1294 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1353

Qy      1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
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Db      1354 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1413

Qy      1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
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Qy      1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1474 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1533

Qy      1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1534 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1593

Qy      1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1594 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1653

Qy      1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1654 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1713

Qy      1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1714 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1773

Qy      1561 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1774 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1833

Qy      1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1834 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1893

Qy      1681 AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1740
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Db       2734 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2793

Qy       2581 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2853

Qy       2641 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2913

Qy       2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2973

Qy       2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAAGAAACAACACTAA 2819
             |||||||||||||||||||||||||| | ||||| ||||||| |||| |||||||||
Db       2974 CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA 3033

Qy       2820 CTCCTCCAATTCCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC 2878
             | ||  ||||||  |||   ||    ||  ||||||||||||||||||||||||||||||
Db       3034 CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC 3093

Qy       2879 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 2938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 3153

Qy       2939 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 2998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 3213

Qy       2999 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3273

Qy       3059 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
             |||||||||||||||||||||||||||||||||||
Db       3274 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3308
```

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RESULT 3
ADA23280
ID   ADA23280 standard; cDNA; 3498 BP.
XX
AC   ADA23280;
XX
DT   20-NOV-2003  (first entry)
XX
DE   cDNA encoding human SECX polypeptide, SEC2.
XX
KW   Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW   SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW   SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW   cardiovascular disease; oncology disease; immune disorder;
KW   autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW   inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW   atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW   trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
```

KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003054514-A1.
XX
PD 20-MAR-2003.
XX
PF 19-SEP-2001; 2001US-00957187.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
XX
PI Shimkets RA, Larochelle WJ;
XX
DR WPI; 2003-540616/51.
DR P-PSDB; ADA23281.
XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 3; Fig 2; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence encodes a
CC SECX polypeptide of the invention.
XX
SQ Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 0 U; 1 Other;

Query Match 98.2%; Score 3038; DB 8; Length 3498;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3072; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 273

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        274 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 453

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 513

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 573

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 633

Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 693

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 753

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 813

Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 873

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 933

Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 993

Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1053

Qy        841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1113

Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1173
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Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1233

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1293

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1353

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1413

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1473

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1533

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1593

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1653

Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1713

Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1773

Qy       1561 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1833

Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1893

Qy       1681 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1953

Qy       1741 TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1954 TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG 2013
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Qy       1801 GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2014 GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG 2073

Qy       1861 GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2074 GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA 2133

Qy       1921 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2134 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 2193

Qy       1981 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2194 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC 2253

Qy       2041 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2254 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC 2313

Qy       2101 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2314 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2373

Qy       2161 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2433

Qy       2221 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2493

Qy       2281 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC 2340
             |||||||||||||||||||||| | |||||||||||| ||||||||||||||||||||
Db       2494 ACCCCAACGCTGCAGCAGAAGCGGGAACCCAGCCGCGGCACCCGCGAGTGGGAGAGGAAC 2553

Qy       2341 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC 2613

Qy       2401 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2673

Qy       2461 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2733

Qy       2521 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2793

Qy       2581 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2853

Qy       2641 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2854 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2913

Qy        2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2914 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2973

Qy        2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAAGAAACAACACTAA 2819
                |||||||||||||||||||||||||| | ||||| |||||||  |||| |||||||||
Db        2974 CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA 3033

Qy        2820 CTCCTCCAATTCCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC 2878
                | ||  ||||||  |||   ||    ||  ||||||||||||||||||||||||||||||
Db        3034 CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC 3093

Qy        2879 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 2938
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3094 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 3153

Qy        2939 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 2998
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3154 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 3213

Qy        2999 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3058
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3214 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3273

Qy        3059 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
                ||||||||||||||||||||||||||||||||||
Db        3274 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3308
```

RESULT 4
ABX71103
ID ABX71103 standard; cDNA; 4280 BP.
XX
AC ABX71103;
XX
DT 05-MAR-2003 (first entry)
XX
DE Novel human cDNA sequence #328.
XX
KW Human; gene; ss; nervous system disorder; peripheral neuropathy;
KW Huntington's disease; amyotrophic lateral sclerosis; haemophilia;
KW neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound;
KW ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke;
KW fibrosis; reperfusion injury; infection; allergic rhinitis; asthma;
KW coagulation disorder; cancer; tumour; inflammatory disease; septic shock;
KW Crohn's disease; anaphylaxis; proliferation; chemotactic;
KW differentiation; stem cell growth factor; haematopoiesis; chemokinetic;
KW haemostatic; antiinflammatory; expressed sequence tag; EST.
XX
OS Homo sapiens.
XX
PN WO200281731-A2.

XX
PD 17-OCT-2002.
XX
PF 29-JAN-2002; 2002WO-US001222.
XX
PR 30-JAN-2001; 2001US-00774528.
XX
PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
XX
PI Tang TY, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2003-058563/05.
XX
PT Novel polypeptide useful for treating neurodegenerative diseases, myeloid
PT or lymphoid cell disorders, bone disorders, mechanical and traumatic
PT disorders, coagulation disorders, and inflammatory diseases.
XX
PS Claim 1; Page; 612pp; English.
XX
CC This invention relates to the cDNA sequences encoding an isolated novel
CC human polypeptide. The protein encoded by the nucleic acid of the
CC invention is useful for treating central and peripheral nervous system
CC diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic
CC lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease,
CC Alzheimer's disease); autoimmune disease (e.g. systemic lupus
CC erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus)
CC ; myeloid or lymphoid cell disorders (e.g. anaemia and thrombocytopaenia)
CC ; wounds, ulcers, burns; bone disorders (e.g. osteoporosis,
CC osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head
CC trauma); lung or liver fibrosis; reperfusion injury in various tissues;
CC bacterial, viral or fungal infections; allergic conditions such as
CC allergic rhinitis, asthma; coagulation disorders (e.g. haemophilia);
CC cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's
CC disease, anaphylaxis). The protein may be used to inhibit the growth,
CC infection or function of infectious agents such as bacteria, fungi,
CC viruses, or to effect bodily characteristics, biorhythms or circadian
CC cycles of rhythms. The protein may also have
CC proliferation/differentiation, stem cell growth factor, haematopoiesis
CC regulation, immune stimulating or suppressing, chemotactic/chemokinetic,
CC haemostatic and thrombolytic, receptor/ligand, and antiinflammatory
CC activities. The cDNA sequences of the invention are useful for expressing
CC recombinant protein for analysis. The present sequence represents a novel
CC human cDNA sequence of the invention, this sequence is an expressed
CC sequence tag (EST) and was identified using subtractive hybridisation
XX
SQ Sequence 4280 BP; 1185 A; 1165 C; 1001 G; 929 T; 0 U; 0 Other;

Query Match 98.0%; Score 3032; DB 7; Length 4280;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 3093; Conservative 0; Mismatches 0; Indels 51; Gaps 1;

Qy 1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 267 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 326

```
Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 386

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 446

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 506

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 566

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 626

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 686

Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 746

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 806

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 866

Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 926

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 986

Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        987 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 1046

Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1047 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1106

Qy        841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1107 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1166

Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
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Db       2007 CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCCTCTTG 2066

Qy       1750 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 1809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2067 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 2126

Qy       1810 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT 1869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2127 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT 2186

Qy       1870 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGAC 1929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2187 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGAC 2246

Qy       1930 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC 1989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2247 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC 2306

Qy       1990 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 2049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2307 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 2366

Qy       2050 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC 2109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2367 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC 2426

Qy       2110 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 2169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2427 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 2486

Qy       2170 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 2229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2487 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 2546

Qy       2230 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG 2289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2547 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG 2606

Qy       2290 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC 2349
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2607 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC 2666

Qy       2350 ATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 2409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2667 ATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 2726

Qy       2410 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2469
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2727 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2786

Qy       2470 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2529
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2787 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2846

Qy       2530 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2589
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2847 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2906
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Qy       2590 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2649
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2907 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2966

Qy       2650 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2709
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2967 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 3026

Qy       2710 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 2769
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3027 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 3086

Qy       2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2829
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3087 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 3146

Qy       2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 2889
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3147 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 3206

Qy       2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3207 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 3266

Qy       2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3009
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3267 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3326

Qy       3010 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3327 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3386

Qy       3070 AAGCCCAATGATGCGTGTACATAA 3093
             |||||||||||||||||||||||
Db       3387 AAGCCCAATGATGCGTGTACATAA 3410
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RESULT 5
ADA23361
ID ADA23361 standard; cDNA; 4250 BP.
XX
AC ADA23361;
XX
DT 20-NOV-2003 (first entry)
XX
DE cDNA encoding human SECX polypeptide, SEC15.
XX
KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW cardiovascular disease; oncology disease; immune disorder;
KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;

KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003054514-A1.
XX
PD 20-MAR-2003.
XX
PF 19-SEP-2001; 2001US-00957187.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
XX
PI Shimkets RA, Larochelle WJ;
XX
DR WPI; 2003-540616/51.
DR P-PSDB; ADA23362.
XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 3; Page 13-14; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence encodes a
CC SECX polypeptide of the invention.
XX
SQ Sequence 4250 BP; 1168 A; 1161 C; 995 G; 926 T; 0 U; 0 Other;

Query Match 97.8%; Score 3025.6; DB 8; Length 4250;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3089; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 309

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        310 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATTGCAACTATACAAAACAGTATCCGGTG 369
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Qy       121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       370 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 429

Qy       181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       430 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 489

Qy       241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       490 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 549

Qy       301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       550 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 609

Qy       361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       610 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 669

Qy       421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       670 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 729

Qy       481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       730 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 789

Qy       541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       790 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 849

Qy       601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       850 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 909

Qy       661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       910 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 969

Qy       721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       970 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 1029

Qy       781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1030 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1089

Qy       841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1090 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1149

Qy       901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1150 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1209
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Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1269

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1329

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1389

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1449

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1509

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1510 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1569

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1629

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1689

Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1749

Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1750 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1809

Qy       1561 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1810 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1869

Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1870 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1929

Qy       1681 AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA-------------- 1726
              ||||||||||||||||||||||||||||||||||||||||||||
Db       1930 AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT 1989

Qy       1727 ------------------------------------ATGGGCATTCCAGTTCCCTCTTG 1749
                                                    ||||||||||||||||||||||
Db       1990 CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCCTCTTG 2049

Qy       1750 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 1809
```

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Db       2890 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2949

Qy       2650 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2950 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 3009

Qy       2710 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 2769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 3069

Qy       2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 3129

Qy       2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 2889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 3189

Qy       2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3190 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 3249

Qy       2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3309

Qy       3010 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3310 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3369

Qy       3070 AAGCCCAATGATGCGTGTACATAA 3093
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Db       3370 AAGCCCAATGATGCGTGTACATAA 3393
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RESULT 6
AAH18729
ID   AAH18729 standard; cDNA; 6060 BP.
XX
AC   AAH18729;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:19004.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-00116126.
XX
PR   29-JUL-1999;   99JP-00248036.
PR   27-AUG-1999;   99JP-00300253.
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PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 19004; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 6060 BP; 1639 A; 1526 C; 1363 G; 1532 T; 0 U; 0 Other;

Query Match 96.0%; Score 2969.6; DB 4; Length 6060;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2994; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

```
Qy         96 CAACTATACAAAACAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACA 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAACTATACAAAACAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACA 60

Qy        156 GAGGCACAGGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGC 215
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         61 GAGGCACAGGCTGGACATCCAGGTGATTATGATCATGAACGGAACCCTCTACATTGCTGC 120

Qy        216 TAGGGACCATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAG 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 TAGGGACCATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAG 180

Qy        276 CAAAAAACTGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAA 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAAAAAACTGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAA 240

Qy        336 ACATAAGGATGAGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATT 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACATAAGGATGAGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATT 300

Qy        396 GTTTGTCTGTGGAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATT 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTTTGTCTGTGGAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATT 360

Qy        456 GGAACCATTCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGC 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GGAACCATTCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGC 420

Qy        516 CAACGTTGCACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGC 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAACGTTGCACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGC 480

Qy        576 CATTGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCA 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CATTGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCA 540

Qy        636 CGATTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATAT 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGATTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATAT 600

Qy        696 CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCC 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTACTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCC 660

Qy        756 AAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACA 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACA 720

Qy        816 GTGGACGTCGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTA 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGGACGTCGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTA 780

Qy        876 TTTCAACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCT 935
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTTCAACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCT 840

Qy        936 GGCAACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACAT 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCAACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACAT 900

Qy        996 GCTTGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCTTGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCAC 960

Qy       1056 CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTC 1020
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Qy       1116 ATCCTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCAT 1175
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCCTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCAT 1080

Qy       1176 CAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCT 1235
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCT 1140

Qy       1236 GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA 1295
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATA 1200

Qy       1296 TCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGC 1355
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCAGAATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGC 1260

Qy       1356 CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA 1415
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAGAATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTA 1320

Qy       1416 CAACTCTG-AAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGC 1474
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CAACTCTGAAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGC 1380

Qy       1475 TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC 1534
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC 1440

Qy       1535 TTGGCCGGTGTGAACGACATGGGAAGTGT-AAAAAAACCTGTATTGCCTCCAGAGACCCA 1593
             |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db       1441 TTGGCCGGTGTGAACGACATGGGAAGTGTAAAAAAAACCTGTATTGCCTCCAGAGACCCA 1500

Qy       1594 TATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTG 1653
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Db       1501 TATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTG 1560

Qy       1654 ACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGGACTGTCACAATTCC 1713
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ACTTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGGACTGTCACAATTCC 1620

Qy       1714 TTTGTGGCACTGAATGGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCG 1773
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1621 TTTGTGGCACTGAATGGGCATTCTAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCG 1680

Qy       1774 ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC 1833
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Db       1681 ACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGAC 1740

Qy       1834 TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG 1893
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAG 1800

Qy       1894 GGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG 1953
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTG 1860
```

```
Qy       1954 GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC 2013
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTAC 1920

Qy       2014 TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC 2073
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTC 1980

Qy       2074 ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGAC 2133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 ACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGAC 2040

Qy       2134 ACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAG 2193
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2194 CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGAC 2253
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       2101 CTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACTAGCACCACCTGGAC 2160

Qy       2254 CTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC 2313
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Db       2161 CTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGC 2220

Qy       2314 CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG 2373
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Db       2221 CGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATG 2280

Qy       2374 CCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCAC 2433
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCAC 2340

Qy       2434 ATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC 2493
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 ATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGAC 2400

Qy       2494 CAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAG 2553
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Db       2401 CAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAG 2460

Qy       2554 TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG 2613
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Db       2461 TATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTG 2520

Qy       2614 GAGAACCTGGACAGCCTGCCCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCG 2673
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GAGAACCTGGACAGCCTGCCCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCG 2580

Qy       2674 GGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCC 2733
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Db       2581 GGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCC 2640

Qy       2734 TACGGGGTTGACTATAAGAGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGCC 2793
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Db       2641 TACGGGGTTGACTATAAGAGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGCC 2700

Qy       2794 ACCACTCTCAAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAG 2853
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2701 ACCACTCTCAAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAG 2760

Qy        2854 AGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTG 2913
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2761 AGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTG 2820

Qy        2914 CACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCC 2973
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Qy        2974 TACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCC 3033
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2881 TACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCC 2940

Qy        3034 CCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2941 CCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATAA 3000
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RESULT 7
AAV44295
ID   AAV44295 standard; cDNA; 3550 BP.
XX
AC   AAV44295;
XX
DT   06-OCT-1998  (first entry)
XX
DE   Human secreted protein clone CJ145_1 cDNA.
XX
KW   Secreted protein; human fetal brain; nutrition; cytokine; stimulant;
KW   cell proliferation; differentiation; immune system; suppressor; ligand;
KW   regulator; hematopoiesis; tissue growth; activin; inhibin; haemostatic;
KW   chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;
KW   anti-inflammatory; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             126. .3053
FT                   /*tag=  a
FT                   /product= "secreted protein"
FT                   /note= "isolated from clone CJ145_1"
XX
PN   WO9827205-A2.
XX
PD   25-JUN-1998.
XX
PF   17-DEC-1997;   97WO-US023330.
XX
PR   18-DEC-1996;   96US-00769192.
PR   13-JAN-1997;   97US-00783401.
PR   16-DEC-1997;   97US-00991872.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Racie LA,  Merberg D,  Treacy M;
```

PI Spaulding V, Agostino MJ;
XX
DR WPI; 1998-362774/31.
DR P-PSDB; AAW64221.
XX
PT New polynucleotides and secreted proteins - obtained from human foetal
PT brain, human adult testes, human adult brain and human adult salivary
PT gland cDNA libraries.
XX
PS Claim 17a; Page 69-71; 110pp; English.
XX
CC This sequence encodes a novel secreted protein from clone CJ145_1
CC isolated from a human fetal brain cDNA library. This protein has
CC applications for nutritional use, cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, hematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombotic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity and other activities
XX
SQ Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 0 U; 1 Other;

Query Match 88.8%; Score 2746.2; DB 2; Length 3550;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 2923; Conservative 1; Mismatches 4; Indels 165; Gaps 1;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 185

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 245

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 305

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 365

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        366 ATAGACACATCACACACSGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 425

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 485

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 545

Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        546 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 605

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 665

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 725

Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 785

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 845

Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 905

Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 965

Qy        841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1025

Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1085

Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1086 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1145

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1205

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1206 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1265

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1325

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1326 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1385

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1386 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1445
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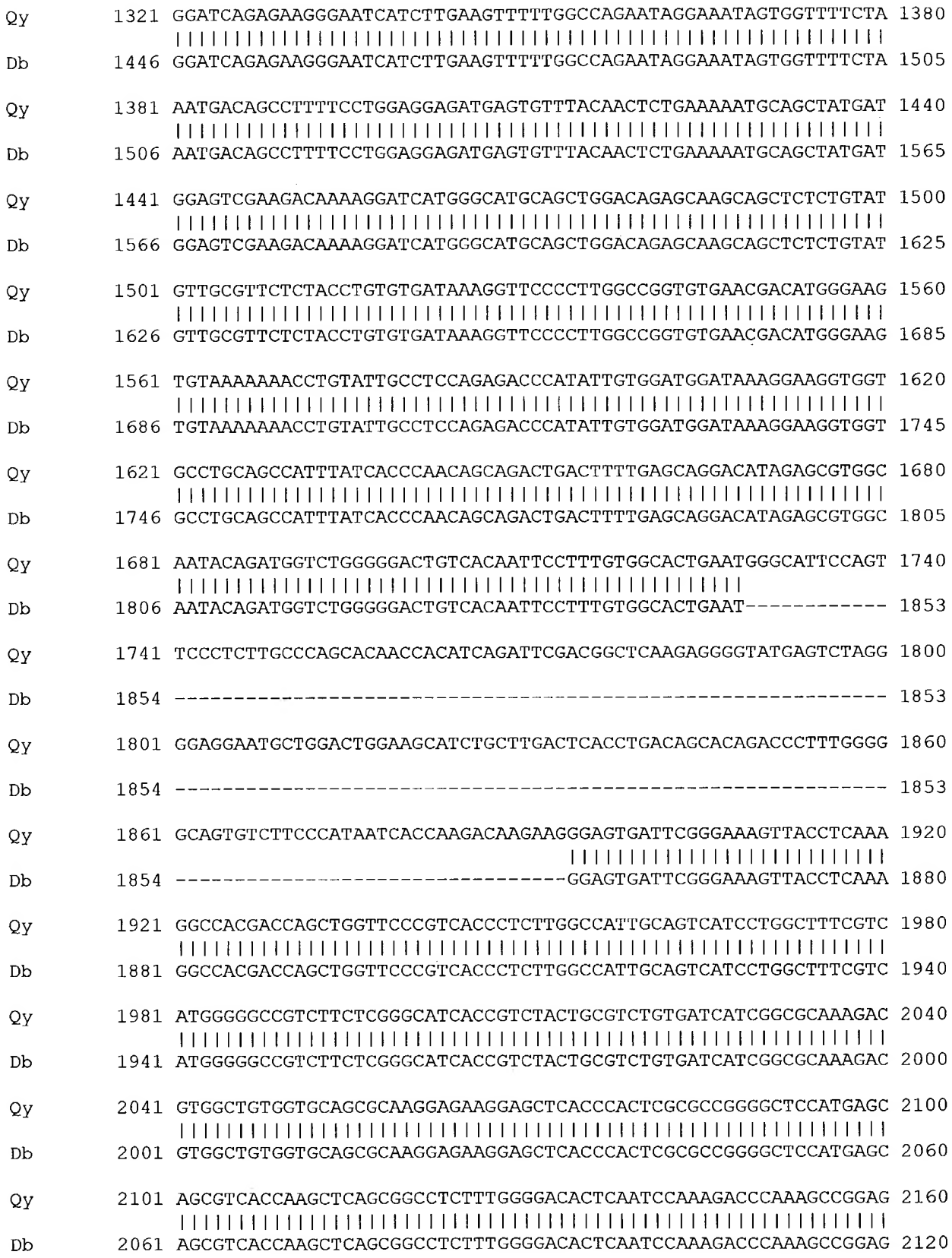

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Qy       2161 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2220
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Db       2121 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2180

Qy       2221 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2181 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2240

Qy       2281 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2241 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC 2300

Qy       2341 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2301 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC 2360

Qy       2401 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2361 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2420

Qy       2461 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2421 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2480

Qy       2521 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2580
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2481 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATTTCAGC 2540

Qy       2581 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2541 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2600

Qy       2641 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2601 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTTTCAGACCGGTTTA 2660

Qy       2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2661 AGCAAGCGGCTGGAAATGCACCACTCCTTTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2720

Qy       2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2721 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC 2780

Qy       2821 TCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2781 TCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG 2840

Qy       2881 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2841 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 2900

Qy       2941 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2901 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTG 2960

Qy       3001 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3060
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2961 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3020

Qy       3061 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
                    ||||||||||||||||||||||||||||||
Db       3021 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3053


RESULT 8
AAF98469
ID   AAF98469 standard; cDNA; 3550 BP.
XX
AC   AAF98469;
XX
DT   07-JUN-2001  (first entry)
XX
DE   Human cDNA clone CJ145_1 sequence SEQ ID 160.
XX
KW   Human; secreted protein; nutrient; cytokine modulator; proliferation;
KW   differentiation; immune system modulator; tissue growth; chemotactic;
KW   haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
KW   haematopoiesis.
XX
OS   Homo sapiens.
XX
PN   WO200119988-A1.
XX
PD   22-MAR-2001.
XX
PF   14-SEP-2000; 2000WO-US025135.
XX
PR   17-SEP-1999;   99US-00398829.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Collins-Racie LA,  Evans C;
PI   Merberg D,  Treacy M,  Bowman MR,  Spaulding V,  Agostino MJ;
XX
DR   WPI; 2001-244801/25.
DR   P-PSDB; AAB90731.
XX
PT   Isolated nucleic acids encoding polypeptides, useful for modulating e.g.
PT   cytokine and cell proliferation/differentiation activity, the immune
PT   system and hematopoiesis regulating activity.
XX
PS   Disclosure; Page 486-487; 557pp; English.
XX
CC   Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
CC   proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
CC   tissue types, and may be used in the prevention, treatment and diagnosis
CC   of diseases associated with inappropriate protein expression. The
CC   polypeptides and nucleic acids may be used as nutrients or to modulate
CC   cytokine and cell proliferation/differentiation activity and may also be
CC   involved in modulation of the immune system. The cDNA sequences,
CC   proteins, their agonists and/or antagonists exhibit haematopoiesis
CC   regulating activity; tissue growth activity; activin/inhibin activity;
CC   chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;
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CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis
CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition
CC activity. Included in the invention are probes represented in AAF98490 -
CC AAF98572 which are specific for the cDNA clones encoding the secreted
CC proteins
XX
SQ Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 0 U; 1 Other;

Query Match 88.8%; Score 2746.2; DB 5; Length 3550;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 2923; Conservative 1; Mismatches 4; Indels 165; Gaps 1;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 185

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 245

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 305

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 365

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Db        366 ATAGACACATCACACACSGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 425

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 485

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 545

Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 605

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 665

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 725

Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 785

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
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Db       1626 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1685

Qy       1561 TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1746 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1805

Qy       1681 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1806 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT------------- 1853

Qy       1741 TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG 1800

Db       1854 ------------------------------------------------------------ 1853

Qy       1801 GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG 1860

Db       1854 ------------------------------------------------------------ 1853

Qy       1861 GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA 1920
                                                 ||||||||||||||||||||||||||
Db       1854 ---------------------------------GGAGTGATTCGGGAAAGTTACCTCAAA 1880

Qy       1921 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1881 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 1940

Qy       1981 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC 2040
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Qy       2041 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC 2100
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Qy       2101 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2160
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Db       2061 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2120

Qy       2161 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2221 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2181 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2240

Qy       2281 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2341 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2301 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC 2360
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Qy       2401 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2361 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2420

Qy       2461 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2421 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2480

Qy       2521 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2580
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db       2481 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATTTCAGC 2540

Qy       2581 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2541 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2600

Qy       2641 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||
Db       2601 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTTTCAGACCGGTTTA 2660

Qy       2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       2661 AGCAAGCGGCTGGAAATGCACCACTCCTTTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2720

Qy       2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2721 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAAC 2780

Qy       2821 TCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2781 TCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCG 2840

Qy       2881 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2841 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 2900

Qy       2941 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2901 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTG 2960

Qy       3001 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2961 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 3020

Qy       3061 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
             ||||||||||||||||||||||||||||||||
Db       3021 ACATCCATGAAGCCCAATGATGCGTGTACATAA 3053
```

RESULT 9
AAA93618
ID   AAA93618 standard; DNA; 3333 BP.
XX
AC   AAA93618;
XX
DT   16-JAN-2001 (first entry)

XX
DE Human semaphorin protein-like splice variant SECX 2864933-2 DNA.
XX
KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200053742-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006280.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 08-MAR-2000; 2000US-0520781P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA;
XX
DR WPI; 2000-594318/56.
DR P-PSDB; AAB23031.
XX
PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.
XX
PS Claim 3; Fig 3; 151pp; English.
XX
CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins of
CC the invention are either secreted or membrane-associated proteins and act
CC as regulator of cellular proliferation and differentiation. SECX proteins
CC or nucleotides are useful for diagnosing the presence of, or
CC predisposition to, a disease associated with altered levels of SECX
CC proteins and nucleotides. The SECX proteins are also useful to screen
CC compounds that modulate SECX activity or expression. The interaction of a
CC SECX protein with other cellular proteins may be useful to modulate the
CC activity of a partner protein, cellular proliferation, cellular
CC differentiation and cell survival. SECX nucleotides are useful for the
CC recombinant expression of SECX protein, and may be used detect SECX mRNA
CC or genetic lesions in the SECX gene. They may also be used to modulate
CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
CC acid sequences are also useful for identifying a cell or tissue type in a
CC biological sample, and in forensic biology. SECX primers or probes are
CC useful for detecting the presence of SECX nucleotides and for screening
CC tissue cultures for contamination. Diseases that may be treated or

CC prevented using SECX proteins or nucleotides include cancer (e.g., colorectal carcinoma, prostate cancer), benign tumours, immune disorders (including autoimmune diseases, transplant rejection, allergies, AIDS), infections, inflammatory disorders, arthritis, haematopoietic disorders, skin disorders, cardiovascular disorders, atherosclerosis, restenosis, neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical or traumatic wounds, spinal cord injury), and skeletal disorders

XX

SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 0 U; 1 Other;

Query Match 87.2%; Score 2698; DB 3; Length 3333;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 2907; Conservative 0; Mismatches 21; Indels 167; Gaps 3;

```
Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 273

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 453

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 513

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 573

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 633

Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 693

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 753

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 813

Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 873
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Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 933

Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 993

Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1053

Qy        841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1113

Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1173

Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1233

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1293

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1353

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1413

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1473

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1533

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1593

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1653

Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1713
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Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1773

Qy       1561 TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1833

Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1893

Qy       1681 AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 AATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT---------- 1941

Qy       1741 TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG 1800

Db       1942 ---------------------------------------------------------- 1941

Qy       1801 GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG 1860

Db       1942 ---------------------------------------------------------- 1941

Qy       1861 GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA 1920
                                                 ||||||||||||||||||||||||||
Db       1942 ----------------------------------GGAGTGATTCGGGAAAGTTACCTCAAA 1968

Qy       1921 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1969 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 2028

Qy       1981 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2029 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC 2088

Qy       2041 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2089 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC 2148

Qy       2101 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2149 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2208

Qy       2161 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2209 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2268

Qy       2221 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2269 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2328

Qy       2281 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC 2340
             |||||||||||||||||||||| | |||||||||||| ||||||||||||||||||||
Db       2329 ACCCCAACGCTGCAGCAGAAGCGGGAACCCAGCCGCGGCACCCGCGAGTGGGAGAGGAAC 2388

Qy       2341 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC 2400
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2389 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC 2448

Qy        2401 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2449 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2508

Qy        2461 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2509 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2568

Qy        2521 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2569 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2628

Qy        2581 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2629 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2688

Qy        2641 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2689 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2748

Qy        2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2749 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2808

Qy        2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAAGAAACAACACTAA 2819
                |||||||||||||||||||||||||| | ||||| |||||||  |||| |||||||||
Db        2809 CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA 2868

Qy        2820 CTCCTCCAATTCCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC 2878
                | ||  |||||| |||   ||    ||  ||||||||||||||||||||||||||||||
Db        2869 CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC 2928

Qy        2879 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 2938
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2929 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 2988

Qy        2939 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 2998
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2989 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 3048

Qy        2999 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3058
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3049 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3108

Qy        3059 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
                |||||||||||||||||||||||||||||||||
Db        3109 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3143


RESULT 10
ADA23282
ID   ADA23282 standard; cDNA; 3333 BP.
XX
AC   ADA23282;
```

XX
DT 20-NOV-2003 (first entry)
XX
DE cDNA encoding human SECX polypeptide, SEC3 #1.
XX
KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW cardiovascular disease; oncology disease; immune disorder;
KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003054514-A1.
XX
PD 20-MAR-2003.
XX
PF 19-SEP-2001; 2001US-00957187.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.
XX
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
XX
PI Shimkets RA, Larochelle WJ;
XX
DR WPI; 2003-540616/51.
DR P-PSDB; ADA23283.
XX
PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.
XX
PS Claim 3; Fig 3; 118pp; English.
XX
CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence encodes a
CC SECX polypeptide of the invention.

XX
SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 0 U; 1 Other;

Query Match 87.2%; Score 2698; DB 8; Length 3333;
Best Local Similarity 93.9%; Pred. No. 0;
Matches 2907; Conservative 0; Mismatches 21; Indels 167; Gaps 3;

```
Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 273

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 453

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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Db        514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 573

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
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Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
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Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
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Db        814 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 873

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
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Db        874 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 933

Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
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Db        934 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 993

Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
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Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
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Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
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Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
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Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
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Qy       1681 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1740
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Qy       2101 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2160
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Qy       2281 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC 2340
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Qy       2461 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2520
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Qy       2999 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3058
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RESULT 11
AAS68807
ID   AAS68807 standard; cDNA; 3039 BP.
XX
AC   AAS68807;
XX
DT   13-FEB-2002 (first entry)
XX
DE   DNA encoding novel human diagnostic protein #4611.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG04620.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 4611; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 U; 0 Other;

Query Match 71.8%; Score 2221.8; DB 5; Length 3039;
Best Local Similarity 91.2%; Pred. No. 0;
Matches 2408; Conservative 0; Mismatches 167; Indels 66; Gaps 2;

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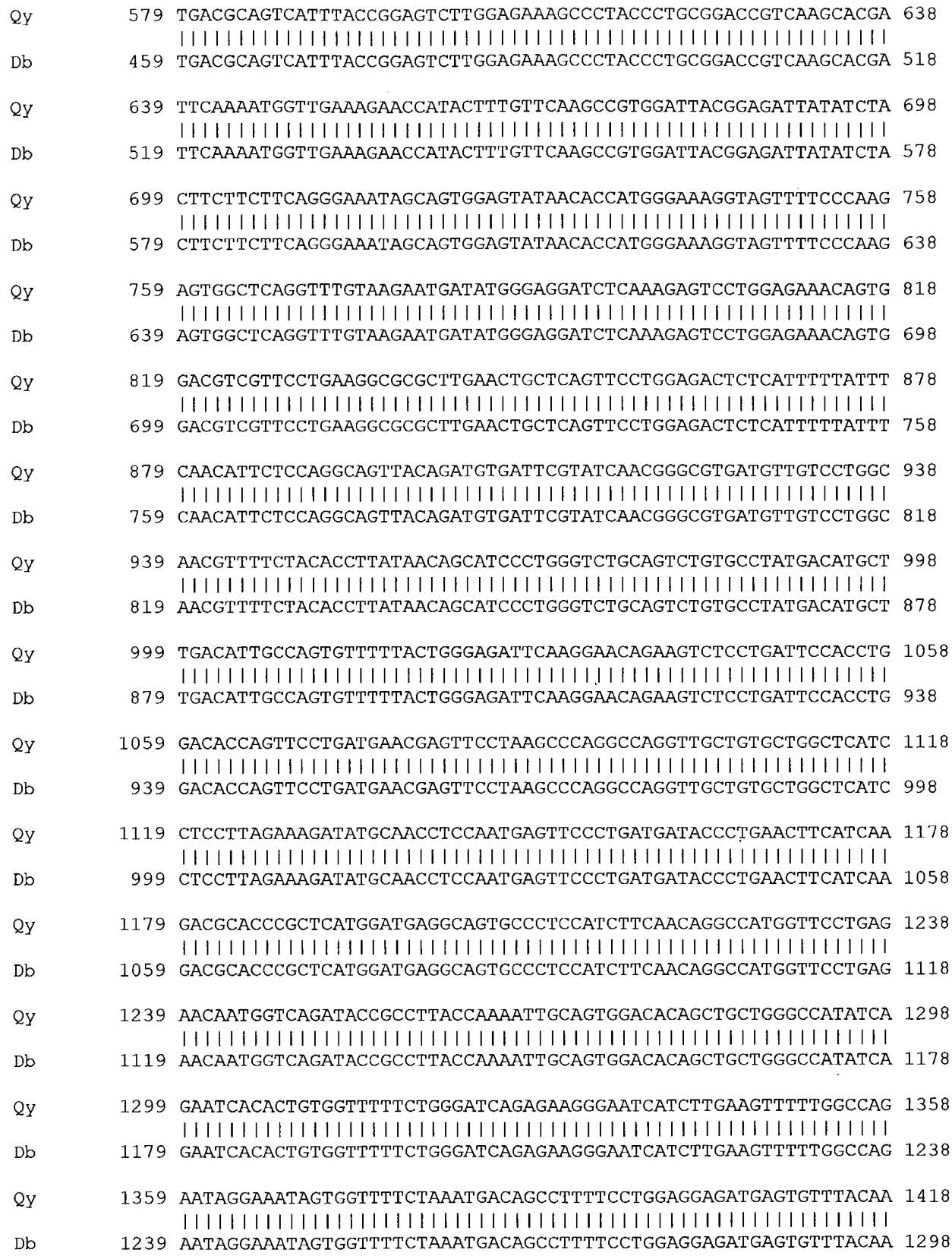
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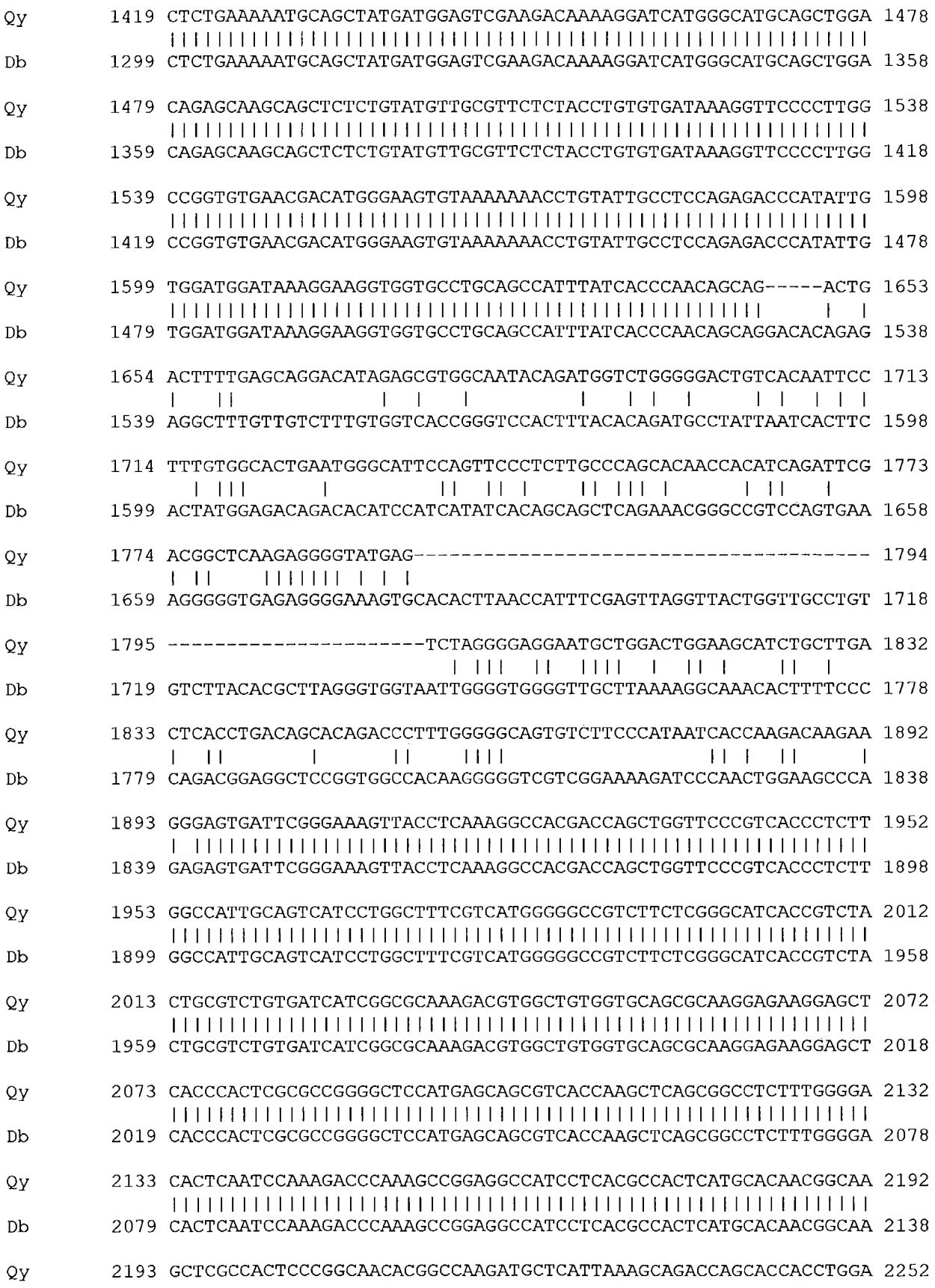

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Qy       2313 CCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACAT 2372
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Qy       2553 GTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGT 2612
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2799 GAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGT 2858

Qy       2913 GCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGC 2972
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2859 GCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGC 2918

Qy       2973 CTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACC 3032
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2919 CTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACC 2978

Qy       3033 CCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATA 3092
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       2979 CCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATA 3038

Qy       3093 A 3093
                |
Db       3039 A 3039
```

RESULT 12
AAS89721
ID AAS89721 standard; cDNA; 3039 BP.
XX
AC AAS89721;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #25525.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG25534.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 25525; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 U; 0 Other;

Query Match 71.8%; Score 2221.8; DB 5; Length 3039;
Best Local Similarity 91.2%; Pred. No. 0;
Matches 2408; Conservative 0; Mismatches 167; Indels 66; Gaps 2;

```
Qy        519 CGTTGCACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCAT 578
              | |  | |||| | ||||||||||||||||||||||||||||||||||||||||||||||
Db        399 CCTGACTCTGTCTCCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCAT 458

Qy        579 TGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGA 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 TGACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGA 518

Qy        639 TTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTA 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 TTCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTA 578

Qy        699 CTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAG 758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 CTTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAG 638

Qy        759 AGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTG 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        639 AGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTG 698

Qy        819 GACGTCGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTT 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 GACGTCGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTT 758

Qy        879 CAACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGC 938
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 CAACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGC 818

Qy        939 AACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCT 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 AACGTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCT 878

Qy        999 TGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTG 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 TGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTG 938

Qy       1059 GACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATC 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 GACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATC 998

Qy       1119 CTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAA 1178
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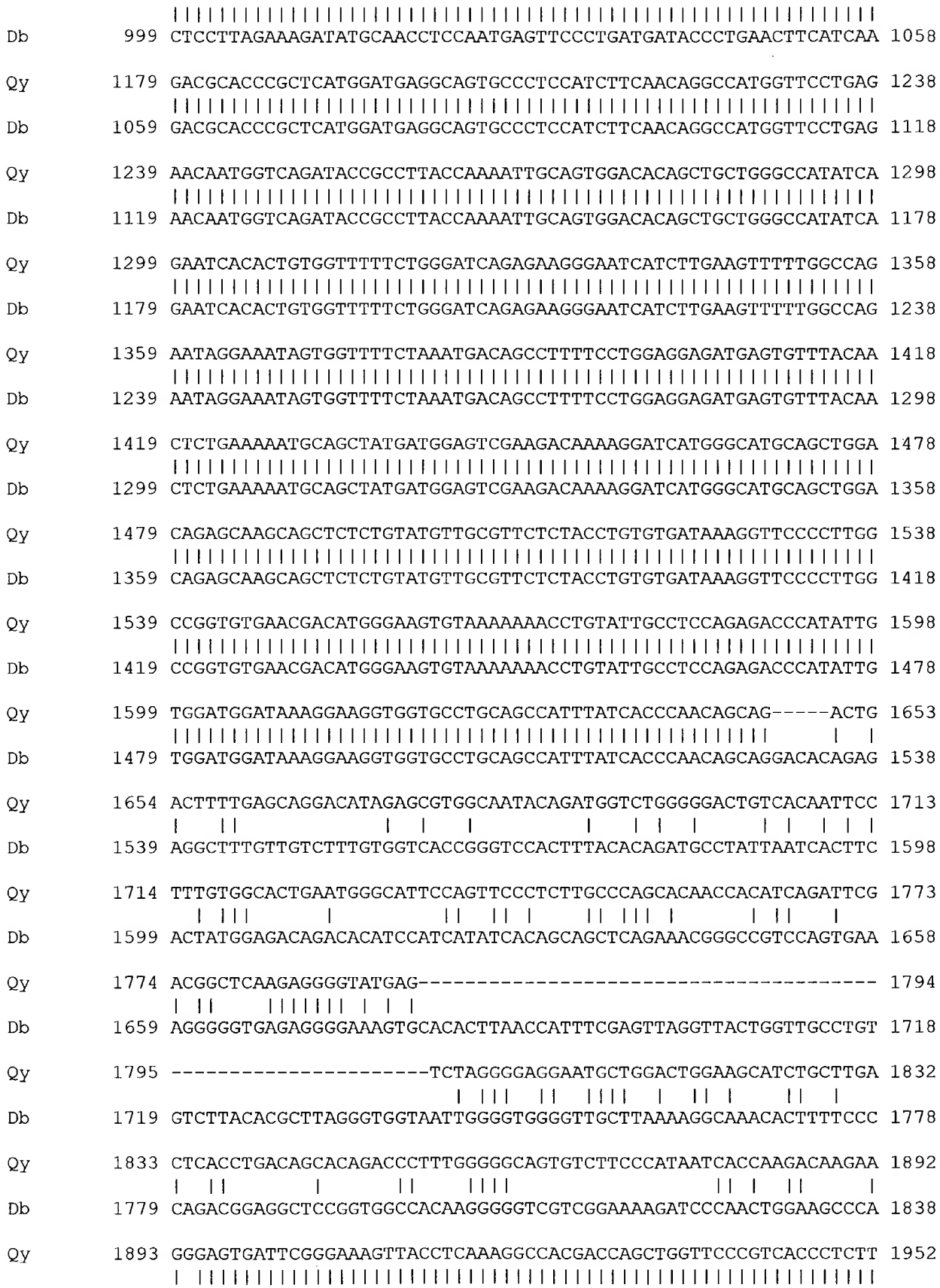

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Db       1839 GAGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTT 1898

Qy       1953 GGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTA 2012
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1899 GGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTA 1958

Qy       2013 CTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCT 2072
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1959 CTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCT 2018

Qy       2073 CACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGA 2132
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2019 CACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGA 2078

Qy       2133 CACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAA 2192
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2079 CACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAA 2138

Qy       2193 GCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGA 2252
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2139 GCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGA 2198

Qy       2253 CCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAG 2312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2199 CCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAG 2258

Qy       2313 CCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACAT 2372
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2259 CCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACAT 2318

Qy       2373 GCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCA 2432
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2319 GCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCA 2378

Qy       2433 CATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGA 2492
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2379 CATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGA 2438

Qy       2493 CCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGA 2552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2439 CCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGA 2498

Qy       2553 GTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGT 2612
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2499 GTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGT 2558

Qy       2613 GGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCC 2672
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2559 GGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCC 2618

Qy       2673 GGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTC 2732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2619 GGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTC 2678

Qy       2733 CTACGGGGTTGACTATAAGAGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGC 2792
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2679 CTACGGGGTTGACTATAAGAGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGC 2738
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Qy       2793 CACCACTCTCAAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCA 2852
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2739 CACCACTCTCAAAAGAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCA 2798

Qy       2853 GAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGT 2912
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2799 GAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGT 2858

Qy       2913 GCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGC 2972
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2859 GCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGC 2918

Qy       2973 CTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACC 3032
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2919 CTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACC 2978

Qy       3033 CCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATA 3092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2979 CCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACATA 3038

Qy       3093 A 3093
             |
Db       3039 A 3039
```

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RESULT 13
AAH17625
ID   AAH17625 standard; cDNA; 3041 BP.
XX
AC   AAH17625;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:17153.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-00116126.
XX
PR   29-JUL-1999;   99JP-00248036.
PR   27-AUG-1999;   99JP-00300253.
PR   11-JAN-2000; 2000JP-00118776.
PR   02-MAY-2000; 2000JP-00183767.
PR   09-JUN-2000; 2000JP-00241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
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DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 17153; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 3041 BP; 804 A; 886 C; 714 G; 637 T; 0 U; 0 Other;

Query Match 70.6%; Score 2182.4; DB 4; Length 3041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        910 CGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAACAGCATCCCT 969
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGTATCAACGGGCATGATGTTGTCCTGGCAACGTTTTCTACACCTTATAACAGCATCCCT 60

Qy        970 GGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACTGGGAGATTC 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACTGGGAGATTC 120

Qy       1030 AAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGAGTTCCTAAG 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGAGTTCCTAAG 180

Qy       1090 CCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACCTCCAATGAG 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACCTCCAATGAG 240

Qy       1150 TTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAGGCAGTGCCC 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAGGCAGTGCCC 300
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Qy       1210 TCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTTACCAAAATT 1269
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Db        301 TCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTTACCAAAATT 360

Qy       1270 GCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCAGAG 1329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCAGAG 420

Qy       1330 AAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGC 1389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTAAATGACAGC 480

Qy       1390 CTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGATGGAGTCGAA 1449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGATGGAGTCGAA 540

Qy       1450 GACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTC 1509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTC 600

Qy       1510 TCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAAAAAA 1569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAGTGTAAAAAA 660

Qy       1570 ACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGC 1629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGC 720

Qy       1630 CATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGAT 1689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGCAATACAGAT 780

Qy       1690 GGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCCTCTTG 1749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGTTCCCTCTTG 840

Qy       1750 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 1809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 900

Qy       1810 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT 1869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT 960

Qy       1870 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGAC 1929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGAC 1020

Qy       1930 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC 1989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC 1080

Qy       1990 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 2049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 1140
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Qy       2050 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC 2109
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Db       1141 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC 1200

Qy       2110 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 2169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 1260

Qy       2170 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 2229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 1320

Qy       2230 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG 2289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG 1380

Qy       2290 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC 2349
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Db       1381 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC 1440

Qy       2350 ATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 2409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 1500

Qy       2410 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2469
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Db       1501 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 1560

Qy       2470 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2529
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 1620

Qy       2530 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2589
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 1680

Qy       2590 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2649
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 1740

Qy       2650 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2709
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 1800

Qy       2710 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 2769
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 1860

Qy       2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2829
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 1920

Qy       2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 2889
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 1980

Qy       2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2040

Qy       2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGGCTGAAGCGTACG 3009
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGGCTGAAGCGTACG 2100

Qy       3010 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 2160

Qy       3070 AAGCCCAATGATGCGTGTACATAA 3093
                ||||||||||||||||||||||||
Db       2161 AAGCCCAATGATGCGTGTACATAA 2184
```

RESULT 14
AAA93630
ID AAA93630 standard; cDNA; 1890 BP.
XX
AC AAA93630;
XX
DT 16-JAN-2001 (first entry)
XX
DE Human semaphorin protein-like splice variant SECX pCR2.1-2864933 cDNA.
XX
KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200053742-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006280.
XX
PR 09-MAR-1999; 99US-0123667P.
PR 08-MAR-2000; 2000US-0520781P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA;
XX
DR WPI; 2000-594318/56.
DR P-PSDB; AAB23043.
XX
PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of

PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders.
XX
PS Claim 3; Fig 15; 151pp; English.
XX
CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins of
CC the invention are either secreted or membrane-associated proteins and act
CC as regulator of cellular proliferation and differentiation. SECX proteins
CC or nucleotides are useful for diagnosing the presence of, or
CC predisposition to, a disease associated with altered levels of SECX
CC proteins and nucleotides. The SECX proteins are also useful to screen
CC compounds that modulate SECX activity or expression. The interaction of a
CC SECX protein with other cellular proteins may be useful to modulate the
CC activity of a partner protein, cellular proliferation, cellular
CC differentiation and cell survival. SECX nucleotides are useful for the
CC recombinant expression of SECX protein, and may be used detect SECX mRNA
CC or genetic lesions in the SECX gene. They may also be used to modulate
CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
CC acid sequences are also useful for identifying a cell or tissue type in a
CC biological sample, and in forensic biology. SECX primers or probes are
CC useful for detecting the presence of SECX nucleotides and for screening
CC tissue cultures for contamination. Diseases that may be treated or
CC prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical
CC or traumatic wounds, spinal cord injury), and skeletal disorders
XX
SQ Sequence 1890 BP; 535 A; 426 C; 463 G; 466 T; 0 U; 0 Other;

Query Match 60.8%; Score 1881.6; DB 3; Length 1890;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1884; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          49 GGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAA 108
               ||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GGATCCGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAA 60

Qy         109 CAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTG 168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTG 120

Qy         169 GACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATT 228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATT 180

Qy         229 TATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACA 288
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACA 240

Qy         289 TGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAG 348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAG 300
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Qy        349 TGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGA 408
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGA 360

Qy        409 ACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGG 468
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGG 420

Qy        469 GATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTG 528
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTG 480

Qy        529 TTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTC 588
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTC 540

Qy        589 ATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGG 648
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGG 600

Qy        649 TTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTC 708
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTC 660

Qy        709 AGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAG 768
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAG 720

Qy        769 GTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTC 828
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTC 780

Qy        829 CTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTC 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTC 840

Qy        889 CAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCT 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCT 900

Qy        949 ACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCC 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCC 960

Qy       1009 AGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTT 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTT 1020

Qy       1069 CCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAA 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAA 1080

Qy       1129 AGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCG 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCG 1140

Qy       1189 CTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTC 1248
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 CTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTC 1200

Qy        1249 AGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACT 1308
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 AGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACT 1260

Qy        1309 GTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAAT 1368
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAAT 1320

Qy        1369 AGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAA 1428
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAA 1380

Qy        1429 TGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGC 1488
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 TGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGC 1440

Qy        1489 AGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAA 1548
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAA 1500

Qy        1549 CGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATA 1608
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 CGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATA 1560

Qy        1609 AAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGAC 1668
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 AAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGAC 1620

Qy        1669 ATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT 1728
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 ATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT 1680

Qy        1729 GGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGG 1788
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 GGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGG 1740

Qy        1789 TATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACA 1848
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 TATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACA 1800

Qy        1849 GACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAA 1908
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1801 GACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAA 1860

Qy        1909 AGTTACCTCAAAGGCCACGACCAGCTGG 1936
                 |||||||||||||||||||||||||| |
Db        1861 AGTTACCTCAAAGGCCACGACCAGCTCG 1888
```

RESULT 15
ADA23359
ID   ADA23359 standard; cDNA; 1890 BP.
XX
AC   ADA23359;

XX

DT 20-NOV-2003 (first entry)

XX

DE cDNA encoding human SECX polypeptide, SEC3 #2.

XX

KW Human; secreted polypeptide; membrane-associated polypeptide; SECX; SEC1;
KW SEC2; SEC3; SEC4; SEC5; SEC6; SEC7; SEC8; SEC9; SEC10; SEC11; SEC12;
KW SEC13; SEC14; SEC15; SECX-associated disorder; lung cancer;
KW cardiovascular disease; oncology disease; immune disorder;
KW autoimmune disease; transplant rejection; allergy; AIDS; infections;
KW inflammatory disorder; arthritis; haematopoietic disorder; skin disorder;
KW atherosclerosis; restenosis; neurological disease; Alzheimer's disease;
KW trauma; wounds; spinal cord injury; skeletal disorder; cytostatic;
KW antiinflammatory; immunosuppressive; anti-HIV; antiarthritic;
KW antiarteriosclerotic; cardiant; neuroprotective; nootropic; vulnerary;
KW antiallergic; cardiant; dermatological; gene; ss.

XX

OS Homo sapiens.

XX

PN US2003054514-A1.

XX

PD 20-MAR-2003.

XX

PF 19-SEP-2001; 2001US-00957187.

XX

PR 09-MAR-1999; 99US-0123667P.
PR 04-JAN-2000; 2000US-0174485P.
PR 08-MAR-2000; 2000US-00520781.
PR 19-SEP-2000; 2000US-0233798P.
PR 20-SEP-2000; 2000US-0234082P.

XX

PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.

XX

PI Shimkets RA, Larochelle WJ;

XX

DR WPI; 2003-540616/51.
DR P-PSDB; ADA23360.

XX

PT New SECX nucleic acids, useful for treating or diagnosing a disorder
PT e.g., lung cancer, cardiovascular and oncology diseases, immune disorder,
PT and autoimmune disease.

XX

PS Claim 3; Page 7; 118pp; English.

XX

CC The present invention relates to the isolation of human secreted or
CC membrane-associated (SECX) polypeptides designated SEC1-SEC15, and the
CC polynucleotide sequences encoding them. Also disclosed is a method for
CC screening for a modulator of activity or latency of SECX. The SECX
CC polypeptide and polynucleotide sequences may be used for treating or
CC preventing SECX-associated disorders such as lung cancer, cardiovascular
CC and oncology diseases, immune disorders, autoimmune diseases, transplant
CC rejection, allergy, AIDS, infections, inflammatory disorders, arthritis,
CC haematopoietic disorders, skin disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g. Alzheimer's disease), trauma, wounds, spinal
CC cord injuries, and skeletal disorders. The present sequence encodes a
CC SECX polypeptide of the invention.

XX
SQ Sequence 1890 BP; 535 A; 426 C; 463 G; 466 T; 0 U; 0 Other;

Query Match 60.8%; Score 1881.6; DB 8; Length 1890;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1884; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          49 GGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAA 108
               ||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GGATCCGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAA 60

Qy         109 CAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTG 168
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTG 120

Qy         169 GACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATT 228
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATT 180

Qy         229 TATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACA 288
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACA 240

Qy         289 TGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAG 348
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAG 300

Qy         349 TGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGA 408
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGA 360

Qy         409 ACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGG 468
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGG 420

Qy         469 GATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTG 528
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTG 480

Qy         529 TTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTC 588
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTC 540

Qy         589 ATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGG 648
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 ATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGG 600

Qy         649 TTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTC 708
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 TTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTC 660

Qy         709 AGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAG 768
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAG 720

Qy         769 GTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTC 828
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        721 GTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTC 780

Qy        829 CTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTC 888
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTC 840

Qy        889 CAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCT 948
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCT 900

Qy        949 ACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCC 1008
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCC 960

Qy       1009 AGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTT 1068
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTT 1020

Qy       1069 CCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAA 1128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAA 1080

Qy       1129 AGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCG 1188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCG 1140

Qy       1189 CTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTC 1248
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Db       1141 CTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTC 1200

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Db       1201 AGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACT 1260

Qy       1309 GTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAAT 1368
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Db       1261 GTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAAT 1320

Qy       1369 AGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAA 1428
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Qy       1429 TGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGC 1488
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Db       1381 TGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGC 1440

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Qy       1549 CGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATA 1608
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Qy       1609 AAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGAC 1668
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Db       1561 AAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGAC 1620
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Qy       1669 ATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGAAT 1728
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Qy       1729 GGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGG 1788
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Qy       1849 GACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAA 1908
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1909 AGTTACCTCAAAGGCCACGACCAGCTGG 1936
             |||||||||||||||||||||||||| |
Db       1861 AGTTACCTCAAAGGCCACGACCAGCTCG 1888
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Search completed: March 26, 2004, 00:01:20
Job time : 1254.51 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 23:24:56 ; Search time 226.203 Seconds
(without alignments)
7588.151 Million cell updates/sec

Title: US-09-856-681A-1
Perfect score: 3093
Sequence: 1 atgaggtcagaagccttgct.....ccaatgatgcgtgtacataa 3093

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1998	64.6	2278	4	US-09-976-594-1002	Sequence 1002, Ap
2	657.4	21.3	1923	4	US-09-653-274-12	Sequence 12, Appl
3	657.4	21.3	3261	4	US-09-653-274-5	Sequence 5, Appli
4	657.4	21.3	3694	4	US-09-653-274-3	Sequence 3, Appli
c 5	604	19.5	846	4	US-09-833-381-920	Sequence 920, App
6	555.4	18.0	3524	4	US-09-077-940A-3	Sequence 3, Appli
7	546.8	17.7	3692	4	US-09-077-940A-1	Sequence 1, Appli
8	443.6	14.3	2790	4	US-09-254-594-5	Sequence 5, Appli
9	443.6	14.3	3432	4	US-09-254-594-4	Sequence 4, Appli
10	369.8	12.0	2787	4	US-09-254-594-2	Sequence 2, Appli
11	369.8	12.0	3195	4	US-09-254-594-1	Sequence 1, Appli

12	368	11.9	591	4	US-09-833-381-112	Sequence 112, App
13	252.6	8.2	4286	4	US-09-976-594-632	Sequence 632, App
14	220	7.1	775	4	US-09-833-381-3	Sequence 3, Appli
15	166	5.4	2854	1	US-08-121-713D-57	Sequence 57, Appl
16	166	5.4	2854	1	US-08-835-268-57	Sequence 57, Appl
17	166	5.4	2854	2	US-09-060-692-57	Sequence 57, Appl
18	166	5.4	2854	3	US-08-833-391-57	Sequence 57, Appl
19	166	5.4	2854	4	US-09-060-610-57	Sequence 57, Appl
20	166	5.4	2854	5	PCT-US94-10151A-57	Sequence 57, Appl
21	146.4	4.7	3560	1	US-08-121-713D-59	Sequence 59, Appl
22	146.4	4.7	3560	1	US-08-835-268-59	Sequence 59, Appl
23	146.4	4.7	3560	2	US-09-060-692-59	Sequence 59, Appl
24	146.4	4.7	3560	3	US-08-833-391-59	Sequence 59, Appl
25	146.4	4.7	3560	4	US-09-060-610-59	Sequence 59, Appl
26	146.4	4.7	3560	5	PCT-US94-10151A-59	Sequence 59, Appl
27	142.2	4.6	2504	1	US-08-121-713D-63	Sequence 63, Appl
28	142.2	4.6	2504	1	US-08-835-268-63	Sequence 63, Appl
29	142.2	4.6	2504	2	US-09-060-692-63	Sequence 63, Appl
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31	142.2	4.6	2504	4	US-09-060-610-63	Sequence 63, Appl
32	142.2	4.6	2504	5	PCT-US94-10151A-63	Sequence 63, Appl
33	126.8	4.1	2670	1	US-08-121-713D-61	Sequence 61, Appl
34	126.8	4.1	2670	1	US-08-835-268-61	Sequence 61, Appl
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37	126.8	4.1	2670	4	US-09-060-610-61	Sequence 61, Appl
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39	125	4.0	2601	1	US-08-121-713D-53	Sequence 53, Appl
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41	125	4.0	2601	2	US-09-060-692-53	Sequence 53, Appl
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44	125	4.0	2601	5	PCT-US94-10151A-53	Sequence 53, Appl
45	121.4	3.9	2898	4	US-09-308-179B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-976-594-1002
; Sequence 1002, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 1002
; LENGTH: 2278

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 411373.7
US-09-976-594-1002

Query Match 64.6%; Score 1998; DB 4; Length 2278;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1998; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db        401 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 460

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Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
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Qy       1981 ATGGGGGCCGTCTTCTCG 1998
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Db       2261 ATGGGGGCCGTCTTCTCG 2278
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RESULT 2
US-09-653-274-12
; Sequence 12, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides
; FILE REFERENCE: HYS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1923

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1923)
US-09-653-274-12

Query Match 21.3%; Score 657.4; DB 4; Length 1923;
Best Local Similarity 64.5%; Pred. No. 1.9e-171;
Matches 1017; Conservative 0; Mismatches 551; Indels 9; Gaps 2;

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Qy     100 TATACAAAACAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGG 159
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Db      61 TATTCAAGGCAATATCCGGTTTTTAGAGGACGCCCTTCAGG------CAATGAATCGCAG 114

Qy     160 CACAGGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGG 219
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Qy     340 AAGGATGAGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTT 399
           || ||||| |||||||||||||| |||||  || |    | |||||||||     | |||
Db     295 AAAGATGAATGCCACAACTTTATCAAAGTATTTGTTCCAAGAAACGATGAGATGGTTTTT 354

Qy     400 GTCTGTGGAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAA 459
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Db     355 GTTTGTGGTACCAATGCATTCAATCCCATGTGTAGATACTACAGGTTGAGTACCTTAGAA 414

Qy     460 CCATTCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAAC 519
                 ||||| ||| | || ||  |||| |||||||||| |||||||| |||  ||||
Db     415 TATGATGGGGAAGAAATTAGTGGCCTGGCAAGATGCCCATTTGATGCCAGACAAACCAAT 474

Qy     520 GTTGCACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATT 579
           ||||| || ||||| ||||| || || || || ||||||||| |||||||| | ||||
Db     475 GTTGCCCTCTTTGCTGATGGGAAGCTGTATTCTGCCACAGTGGCTGACTTCTTGGCCAGC 534

Qy     580 GACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGAT 639
           || || || ||||| || ||  | || ||  |  || |||| || ||  | ||  | |||
Db     535 GATGCCGTTATTTATCGAAGCATGGGTGATGGATCTGCCCTTCGCACAATAAAATATGAT 594

Qy     640 TCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTAC 699
           || |||||| | ||||| ||| ||||| |||| ||| | || || ||| | ||| ||||
Db     595 TCCAAATGGATAAAAGAGCCACACTTTCTTCATGCCATAGAATATGGAAACTATGTCTAT 654

Qy     700 TTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGA 759
           ||||||||  | ||||| || || ||  |||| |   | || ||||  || |   |  |
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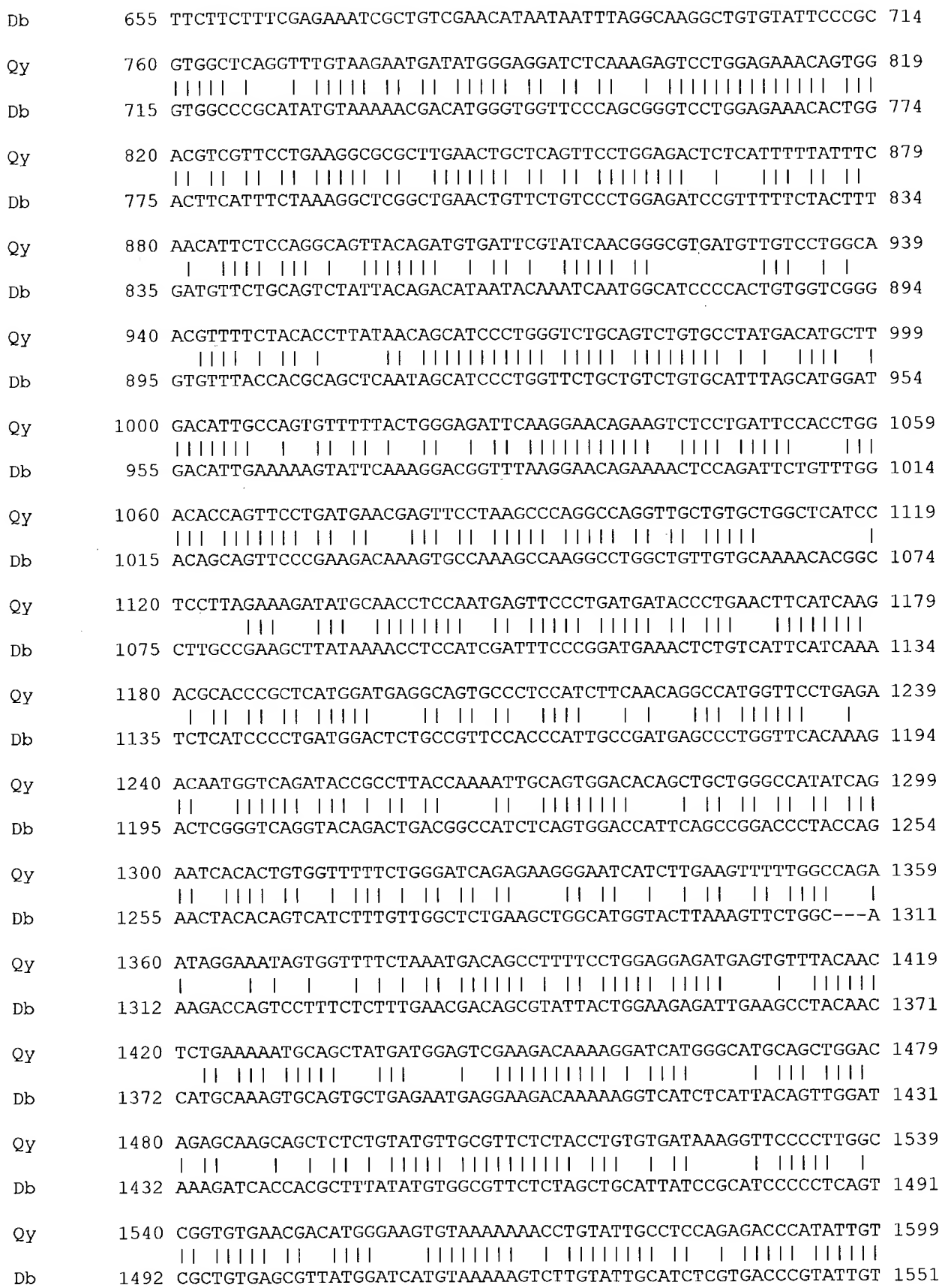

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Qy       1600 GGATGGATAAAGGAAGG 1616
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Db       1552 GGCTGGTTAAGCCAGGG 1568
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RESULT 3
US-09-653-274-5
; Sequence 5, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides
; FILE REFERENCE: HYS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-653-274-5

Query Match 21.3%; Score 657.4; DB 4; Length 3261;
Best Local Similarity 64.5%; Pred. No. 2.6e-171;
Matches 1017; Conservative 0; Mismatches 551; Indels 9; Gaps 2;

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Qy         40 CACTTTGCTGGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAAC 99
              || ||    |  |   | || || ||||||  ||| ||  | | || |    |     ||
Db         49 CAGTTGAGGGCAGTCAGCTTTCCTGAAGATGATGAACCCCTTAATACTGTCGACTATCAC 108

Qy        100 TATACAAAACAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGG 159
              ||| |||  || |||||||| |||   || | |    ||||      ||    |  |  |
Db        109 TATTCAAGGCAATATCCGGTTTTTAGAGGACGCCCTTCAGG------CAATGAATCGCAG 162

Qy        160 CACAGGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGG 219
              |||||||||||| | ||| ||||  |||  ||    |  || || || |||||||  |||
Db        163 CACAGGCTGGACTTTCAGCTGATGTTGAAAATTCGAGACACACTTTATATTGCTGGCAGG 222

Qy        220 GACCATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAA 279
              || ||  |||||||  ||  |  || |   |   | ||    |||| |       | |||
Db        223 GATCAAGTTTATACAGTAAACTTAAATGAAATGCCCAAAACAGAAGTAATACCCAACAAG 282

Qy        280 AAACTGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACAT 339
              ||||||||||||  ||| |||||    |||  ||| |  ||    ||||| || || |||
Db        283 AAACTGACATGGCGATCAAGACAACAGGATCGAGAAAACTGTGCTATGAAAGGCAAGCAT 342
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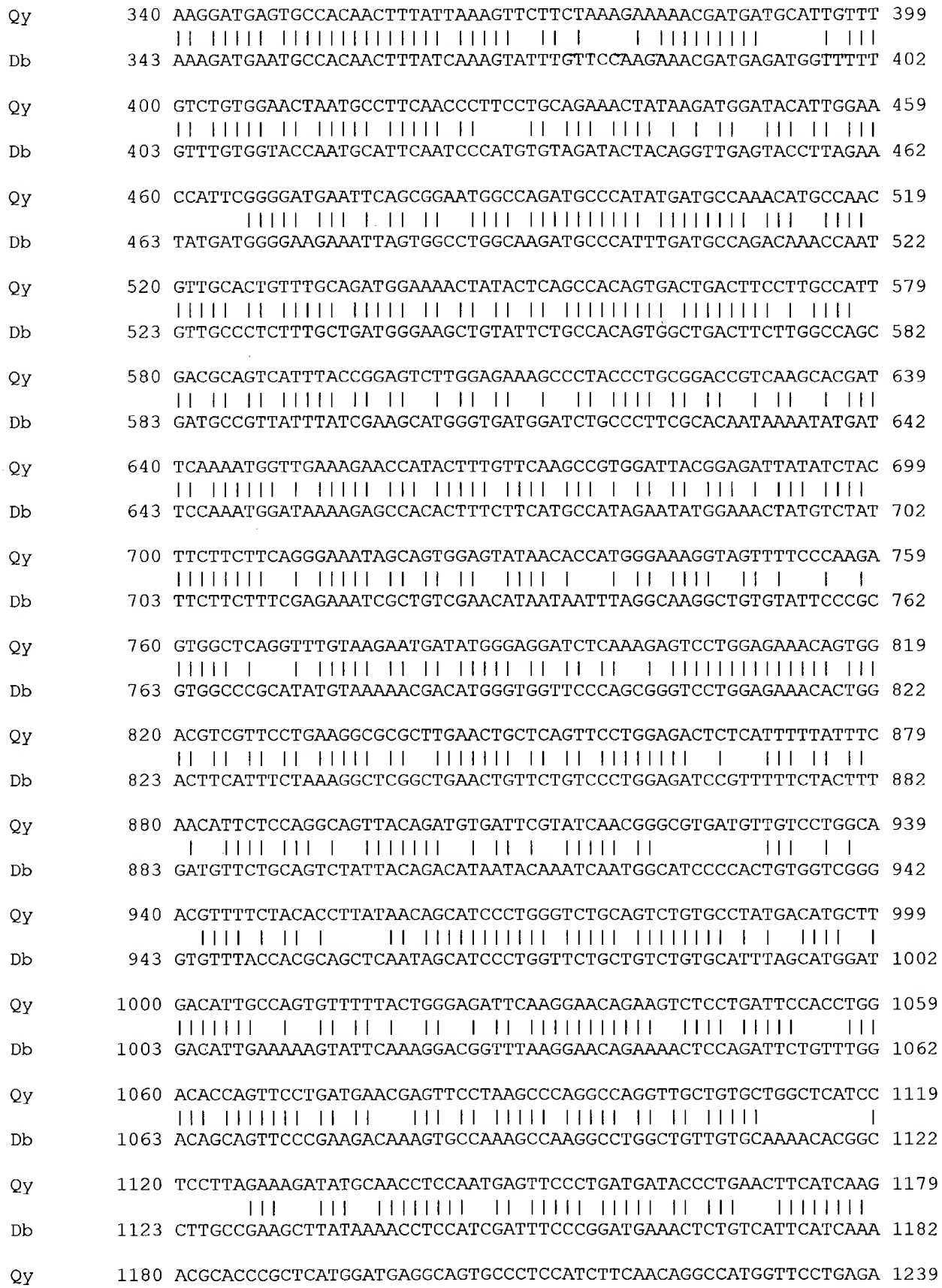

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Db       1183 TCTCATCCCCTGATGGACTCTGCCGTTCCACCCATTGCCGATGAGCCCTGGTTCACAAAG 1242

Qy       1240 ACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAG 1299
Db       1243 ACTCGGGTCAGGTACAGACTGACGGCCATCTCAGTGGACCATTCAGCCGGACCCTACCAG 1302

Qy       1300 AATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGA 1359
Db       1303 AACTACACAGTCATCTTTGTTGGCTCTGAAGCTGGCATGGTACTTAAAGTTCTGGC---A 1359

Qy       1360 ATAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAAC 1419
Db       1360 AAGACCAGTCCTTTCTCTTTGAACGACAGCGTATTACTGGAAGAGATTGAAGCCTACAAC 1419

Qy       1420 TCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGAC 1479
Db       1420 CATGCAAAGTGCAGTGCTGAGAATGAGGAAGACAAAAAGGTCATCTCATTACAGTTGGAT 1479

Qy       1480 AGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGC 1539
Db       1480 AAAGATCACCACGCTTTATATGTGGCGTTCTCTAGCTGCATTATCCGCATCCCCCTCAGT 1539

Qy       1540 CGGTGTGAACGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGT 1599
Db       1540 CGCTGTGAGCGTTATGGATCATGTAAAAAGTCTTGTATTGCATCTCGTGACCCGTATTGT 1599

Qy       1600 GGATGGATAAAGGAAGG 1616
Db       1600 GGCTGGTTAAGCCAGGG 1616
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RESULT 4
US-09-653-274-3
; Sequence 3, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
;  APPLICANT:  Boyle, Bryan J
;  APPLICANT:  Yeung, George Y
;  APPLICANT:  Arterburn, Matthew C
;  APPLICANT:  Mize, Nancy K
;  APPLICANT:  Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION:  Methods and Maaterials Relating to Semaphorin-Like
;  TITLE OF INVENTION:  Polypeptides and Polynucleotides
;  FILE REFERENCE:  HYS-23
;  CURRENT APPLICATION NUMBER: US/09/653,274
;  CURRENT FILING DATE:  2000-08-31
;  PRIOR APPLICATION NUMBER:  09/491,404
;  PRIOR FILING DATE:  2000-01-10
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3694
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (434)..(3694)
US-09-653-274-3

Query Match 21.3%; Score 657.4; DB 4; Length 3694;
Best Local Similarity 64.5%; Pred. No. 2.8e-171;
Matches 1017; Conservative 0; Mismatches 551; Indels 9; Gaps 2;

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Qy        40 CACTTTGCTGGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAAC 99
             || ||    |  |   | || || ||||||  ||| ||  | | || |    |     ||
Db       482 CAGTTGAGGGCAGTCAGCTTTCCTGAAGATGATGAACCCCTTAATACTGTCGACTATCAC 541

Qy       100 TATACAAAACAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGG 159
             ||| |||  || ||||||||| |||   || | |    ||||      ||    |  |  |
Db       542 TATTCAAGGCAATATCCGGTTTTTAGAGGACGCCCTTCAGG------CAATGAATCGCAG 595

Qy       160 CACAGGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGG 219
             |||||||||||| | ||| ||||  |||  ||    |  || || || |||||||  |||
Db       596 CACAGGCTGGACTTTCAGCTGATGTTGAAAATTCGAGACACACTTTATATTGCTGGCAGG 655

Qy       220 GACCATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAA 279
             || ||  ||||||| ||  |  || |   |   | ||    |||| |       | |||
Db       656 GATCAAGTTTATACAGTAAACTTAAATGAAATGCCCAAAACAGAAGTAATACCCAACAAG 715

Qy       280 AAACTGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACAT 339
             ||||||||||||  ||| |||||    |||  ||| |  ||    ||||| || || |||
Db       716 AAACTGACATGGCGATCAAGACAACAGGATCGAGAAAACTGTGCTATGAAAGGCAAGCAT 775

Qy       340 AAGGATGAGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTT 399
             || ||||| |||||||||||||| |||||  || |    | |||||||||     | |||
Db       776 AAAGATGAATGCCACAACTTTATCAAAGTATTTGTTCCAAGAAACGATGAGATGGTTTTT 835

Qy       400 GTCTGTGGAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAA 459
             || ||||| || ||||| ||||| ||    || ||| |||| | | ||  ||| || |||
Db       836 GTTTGTGGTACCAATGCATTCAATCCCATGTGTAGATACTACAGGTTGAGTACCTTAGAA 895

Qy       460 CCATTCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAAC 519
                 ||||| ||| | || ||  |||| |||||||||| |||||||| |||  ||||
Db       896 TATGATGGGGAAGAAATTAGTGGCCTGGCAAGATGCCCATTTGATGCCAGACAAACCAAT 955

Qy       520 GTTGCACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATT 579
             ||||| || ||||| ||||| || || || || ||||||||| |||||||| | ||||
Db       956 GTTGCCCTCTTTGCTGATGGGAAGCTGTATTCTGCCACAGTGGCTGACTTCTTGGCCAGC 1015

Qy       580 GACGCAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGAT 639
             || || || ||||| || ||  | || ||  |  || |||| || ||  | ||  | |||
Db      1016 GATGCCGTTATTTATCGAAGCATGGGTGATGGATCTGCCCTTCGCACAATAAAATATGAT 1075

Qy       640 TCAAAATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTAC 699
             || |||||| | ||||| ||| ||||| |||| ||| | || || ||| | ||| ||||
Db      1076 TCCAAATGGATAAAAGAGCCACACTTTCTTCATGCCATAGAATATGGAAACTATGTCTAT 1135

Qy       700 TTCTTCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGA 759
             ||||||||  | ||||| || || ||  |||| |   | || ||||  || |   |  |
Db      1136 TTCTTCTTTCGAGAAATCGCTGTCGAACATAATAATTTAGGCAAGGCTGTGTATTCCCGC 1195
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Db       2033 GGCTGGTTAAGCCAGGG 2049


RESULT 5
US-09-833-381-920/c
; Sequence 920, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
;  FILE REFERENCE: 5800-119
;  CURRENT APPLICATION NUMBER: US/09/833,381
;  CURRENT FILING DATE:  2001-04-11
;  PRIOR APPLICATION NUMBER: 09/516,448
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 2050
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 920
;   LENGTH: 846
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-833-381-920

  Query Match             19.5%;  Score 604;  DB 4;  Length 846;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-157;
  Matches  604;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 545

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 485

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 425

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 365

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 305

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 245

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 185

Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
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Qy         481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         124 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 65

Qy         541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          64 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 5

Qy         601 CTTG 604
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Db           4 CTTG 1


RESULT 6
US-09-077-940A-3
; Sequence 3, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
;  APPLICANT: KIMURA, Toru et al.
;  TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
;  FILE REFERENCE: 0020-4426P
;  CURRENT APPLICATION NUMBER: US/09/077,940A
;  CURRENT FILING DATE:  1998-06-05
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 3524
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(38)
;   OTHER INFORMATION:
;   NAME/KEY: 3'UTR
;   LOCATION: (2706)..(3524)
;   OTHER INFORMATION:
;   NAME/KEY: CDS
;   LOCATION: (39)..(2702)
;   OTHER INFORMATION:
US-09-077-940A-3

  Query Match             18.0%;  Score 555.4;  DB 4;  Length 3524;
  Best Local Similarity   60.0%;  Pred. No. 4.3e-143;
  Matches 1026;  Conservative    0;  Mismatches  656;  Indels   27;  Gaps    5;

Qy          13 GCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTCCCAGAAGATTCT 72
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Db          72 GCCCTGCTGCTTCTGCTGCTGCTACTGGGGGGCGCCCACGGCCTCTTTCCTGAGGACCCG 131

Qy          73 GAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTGTTTGTGGGCCAC 132
                 |||  | ||  |  | |   |  ||||    || || ||||| ||||||||||||  |
Db         132 CCGCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCACTATCCCGTGTTTGTGGGCAGC 191

Qy         133 AAGCCAGGACGGAACACCAC------ACAGAGGCACAGGCTGGACATCCAGATGATTATG 186
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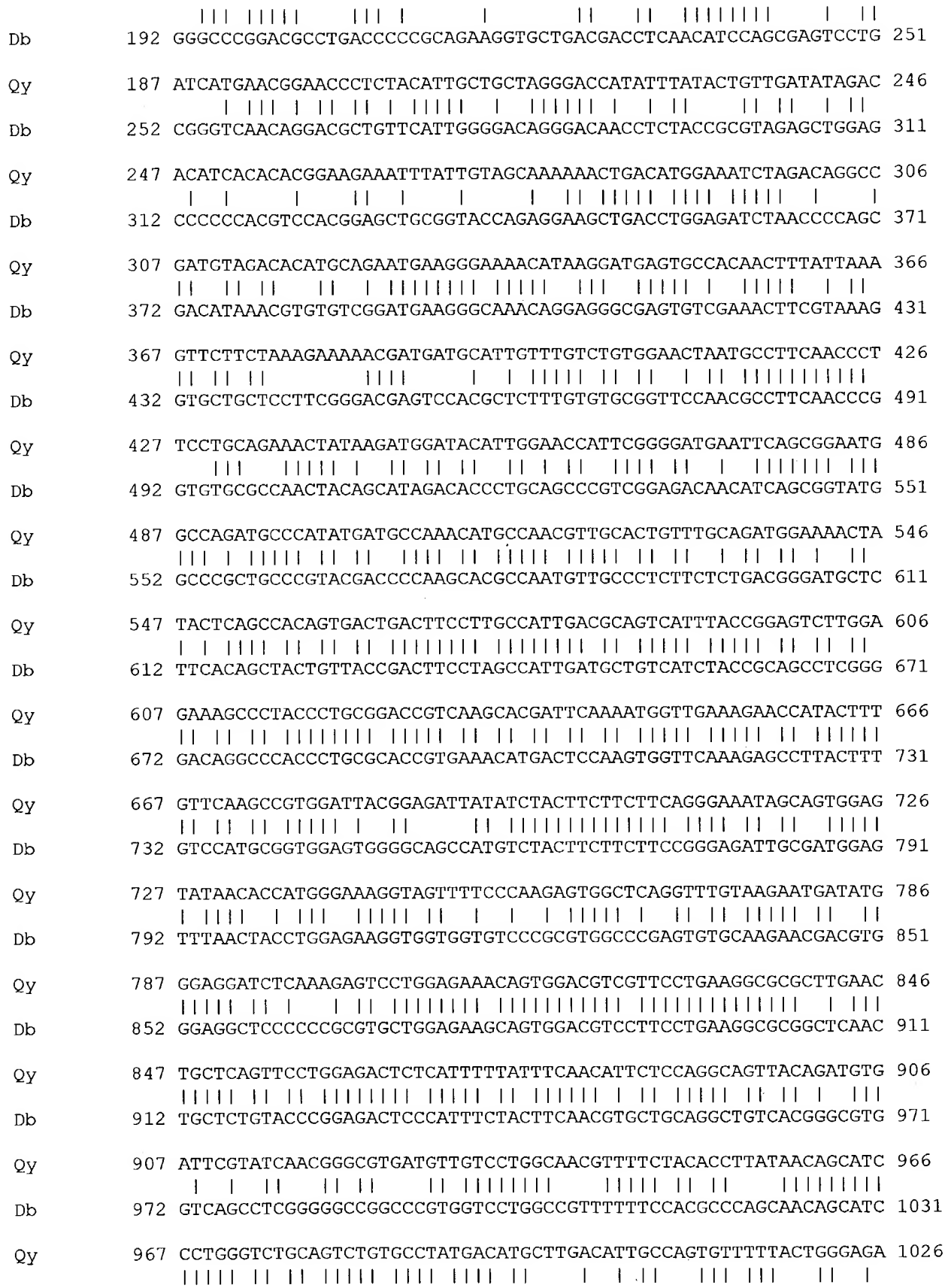

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              |||   || |||||||| || || |||| |||||| || || || || || |  || |||
Db       1092 TTCCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCCGGTGCCGGAGGATCAGGTGCCT 1151

Qy       1087 AAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACCTCCAAT 1146
                ||| |||| || ||||      || || || ||          ||     ||||||
Db       1152 CGACCCCGGCCCGGGTGCT------GCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGC 1205

Qy       1147 GAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAGGCAGTG 1206
              |  || || ||||| | ||| |||||  ||||||| ||||| || ||||| ||||| |||
Db       1206 GCCTTGCCGGATGACATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTG 1265

Qy       1207 CCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTTACCAAA 1266
              |||||  |   | |   ||| ||| ||||| | ||  || | ||  |||  || ||   |
Db       1266 CCCTCGCTGGGCCATGCGCCCTGGATCCTGCGGACCCTGATGAGGCACCAGCTGACTCGA 1325

Qy       1267 ATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTGGGATCA 1326
               | || ||||||   |  || || || |     || || || || || || ||||| ||
Db       1326 GTGGCTGTGGACGTGGGAGCCGGCCCCTGGGGCAACCAGACCGTTGTCTTCCTGGGTTCT 1385

Qy       1327 GAGAAGGGAATCATCTTGAAGTTTTT------GGCCAGAATAGGAAATAGTGGTTTTCTA 1380
              |||  ||| |   || | |||||  |      | |||      | |     ||
Db       1386 GAGGCGGGGACGGTCCTCAAGTTCCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT 1445

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAG------C 1434
                  |||  | |||||||||||| |       |||    | || |  ||  |      |
Db       1446 GGGCTCAGTGTCTTCCTGGAGGAGTTTGAGACCTACCGGCCGGACAGGTGTGGACGGCCC 1505

Qy       1435 TATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCT 1494
                | ||| |    ||   |  || |  || || || |||||||  |||     |
Db       1506 GGCGGTGGCGAGACAGGGCAGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCGGGGGGC 1565

Qy       1495 CTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACAT 1554
              |||   | ||| ||| |   ||| ||| |    || ||  | |  || ||  | |   |
Db       1566 CTGCTGGCTGCCTTCCCCCGCTGCGTGGTCCGAGTGCCTGTGGCTCGCTGCCAGCAGTAC 1625

Qy       1555 GGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAA 1614
                |  |||||  || | |||||| | |      ||||| || || || |||      ||
Db       1626 TCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGCGGGTGGGCCCCCGAC 1685

Qy       1615 GGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAG 1674
              ||     |||||| |    |    ||   || ||||    | ||||||||||||  |
Db       1686 GGCT---CCTGCATCTTCCTCAGCCCGGGCACCAGAGCCGCCTTTGAGCAGGACGTGTCC 1742

Qy       1675 CGTGGCAATACAGATGGTCTGGGGGACTG 1703
               | | ||  ||    ||  | ||||||||
Db       1743 GGGGCCAGCACCTCAGGCTTAGGGGACTG 1771
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RESULT 7
US-09-077-940A-1
; Sequence 1, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.

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;  TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
;  FILE REFERENCE: 0020-4426P
;  CURRENT APPLICATION NUMBER: US/09/077,940A
;  CURRENT FILING DATE:  1998-06-05
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 3692
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(18)
;   OTHER INFORMATION:
;   NAME/KEY: CDS
;   LOCATION: (19)..(2682)
;   OTHER INFORMATION:
;   NAME/KEY: 3'UTR
;   LOCATION: (2683)..(3653)
;   OTHER INFORMATION:
;   NAME/KEY: polyA_site
;   LOCATION: (3654)..(3692)
;   OTHER INFORMATION:
US-09-077-940A-1

  Query Match             17.7%;  Score 546.8;  DB 4;  Length 3692;
  Best Local Similarity   60.3%;  Pred. No. 1.1e-140;
  Matches 1006;  Conservative    0;  Mismatches  632;  Indels   30;  Gaps    5;

Qy          57 TTTCCCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCC 116
               ||||||||| ||  |    ||| ||||| |  | |   |  ||||    |  || || ||
Db          99 TTTCCCAGATGAACCACCTCCACTCAGTGTGGCTCCCAGGGACTACCTGAGCCACTACCC 158

Qy         117 GGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGC------ACAGGCTGGA 170
                ||||| ||||||  |  ||| || ||    ||| |      |       |    ||  |
Db         159 CGTGTTCGTGGGCAGCGGGCCTGGTCGTCTGACCCCTGCAGAGGGTGCTGAGGACCTCAA 218

Qy         171 CATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTA 230
               ||||||||   |  |     | ||| | || || | ||| |  |  || ||| |  | ||
Db         219 CATCCAGAGAGTGCTACGTGTTAACAGGACACTGTTCATCGGGGACAGAGACAACCTGTA 278

Qy         231 TACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATG 290
                   || ||  | ||  ||||     |    ||  |    | |      || || || ||
Db         279 CCAAGTAGAACTGGAGCCATCCACATCCACGGAGCTGCGGTATCAGCGGAAGCTTACCTG 338

Qy         291 GAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTG 350
               |  || |  |     ||  | ||    ||  | |||||||| || ||  ||| ||||||
Db         339 GCGCTCCAACCCCAGTGACATCGATGTGTGTCGGATGAAGGGCAAGCAAGAGGGTGAGTG 398

Qy         351 CCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAAC 410
                |  |||||| | || || || ||        ||||     |  | || || || ||  |
Db         399 TCGGAACTTTGTCAAGGTGCTCCTGCTTCGTGACGAATCCACGCTCTTCGTGTGCGGCTC 458

Qy         411 TAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGA 470
                ||||| ||||| ||   |||    || || |  ||||| ||| || | |   | || ||
Db         459 CAATGCATTCAATCCCATCTGTGCCAATTACAGTATGGACACACTGCAGCTTCTTGGAGA 518
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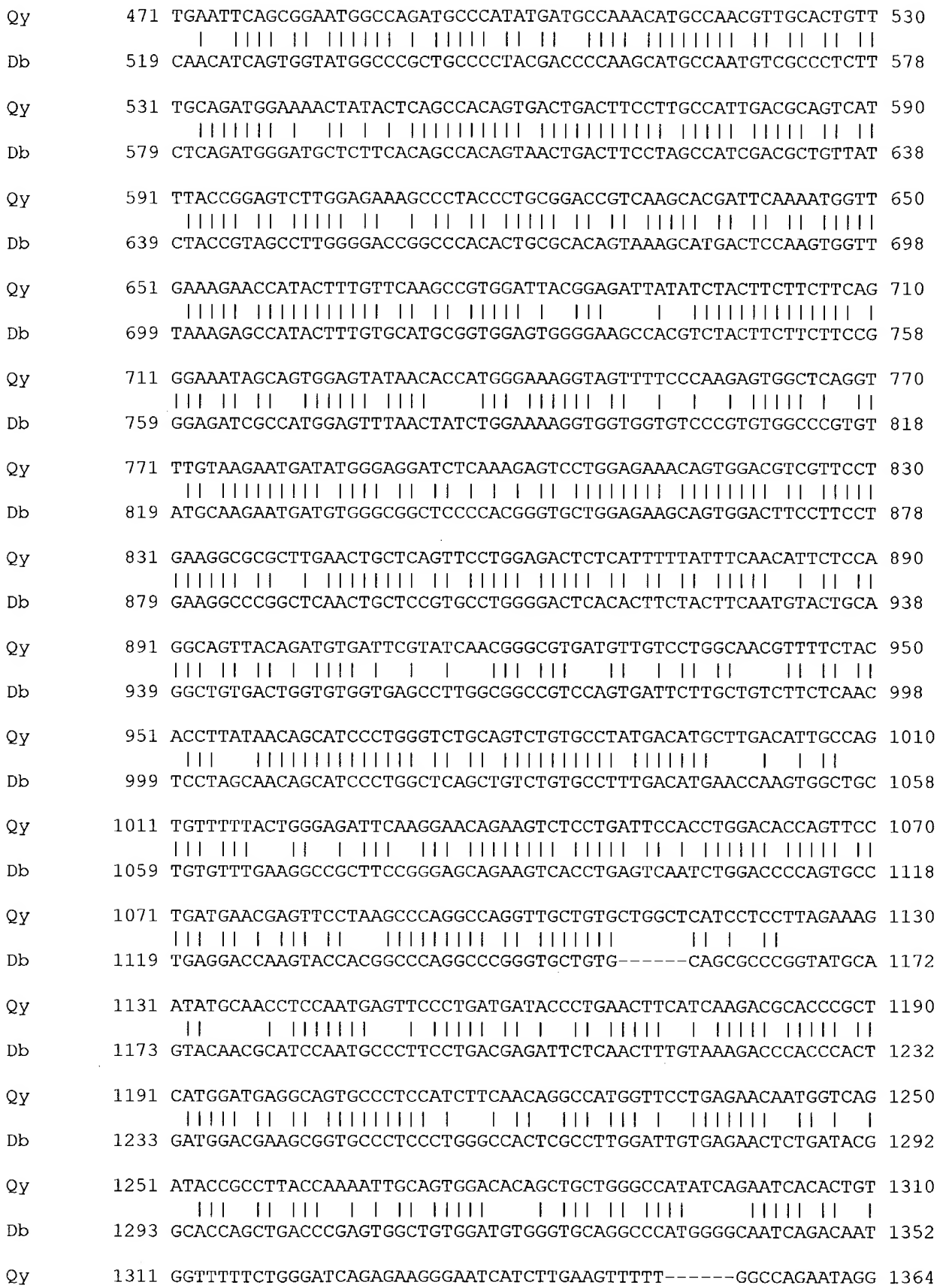

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                 || || || || || |||   || |   || | || ||  |      | |||      |
Db       1353 AGTCTTCCTTGGCTCTGAGGTTGGCACAGTCCTCAAATTCCTTGTGAAGCCCAATGCCAG 1412

Qy       1365 AAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTT---------A 1415
                    ||      |    |||| | ||  |||||||| |       |         |
Db       1413 TGTCTCAGGGACCACAGGGCCCAGCATCTTTTTGGAGGAGTTTGAGACCTACCGGCCAGA 1472

Qy       1416 CAACTCTGAAAAATGCAGCTATGATGGAGTCGAAGACAAAAGGATCATGGGCATGCAGCT 1475
                 ||  | || |  || ||||  || ||| |     |   || |  |  || || || ||||
Db       1473 CAGGTGTGGACGATCCAGCAGTGCTGGTGAGTGGGGACAACGACTTCTGAGCCTGGAGCT 1532

Qy       1476 GGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCT 1535
                 ||    ||     |    |||   |  || ||| |   ||||||| |    |||||  |
Db       1533 AGATGCTGCCTCAGGTGGCCTGCTGGCAGCCTTCCCCCGCTGTGTGGTTCGTGTTCCTGT 1592

Qy       1536 TGGCCGGTGTGAACGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATA 1595
                 || ||| ||  | |   |   |  ||| |  || | ||| |||| |  |  ||| |||||
Db       1593 TGCCCGCTGCCAGCTGTACTCGGGGTGCATGAAGAACTGCATTGGCAGCCAAGATCCATA 1652

Qy       1596 TTGTGGATGGATAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGAC 1655
                 || || |||      ||   |||  |||||| |    |   |||    | |||    ||
Db       1653 CTGCGGGTGGGCCCCCGA---TGGCTCCTGCATCTTCCTCAGACCAGGAACCAGTGCCAC 1709

Qy       1656 TTTTGAGCAGGACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTG 1703
                 |||||||| ||  |     | | ||  ||   |||  | || |||||
Db       1710 GTTTGAGCAAGATGTGTCCGGGGCCAGCACCTCTGGCTTAGGTGACTG 1757
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RESULT 8
US-09-254-594-5
; Sequence 5, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
;  APPLICANT:  KIMURA, Toru
;  APPLICANT:  KIKUCHI, Kaoru
;  TITLE OF INVENTION:   NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
;  FILE REFERENCE:   0020-4527P
;  CURRENT APPLICATION NUMBER: US/09/254,594
;  CURRENT FILING DATE:  1999-05-11
;  NUMBER OF SEQ ID NOS:   13
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 2790
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Tissue Type: Child Brain
;   NAME/KEY: CDS
;   LOCATION: (1)..(2790)
;   OTHER INFORMATION: Identification Method: E
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-5
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Query Match 14.3%; Score 443.6; DB 4; Length 2790;
Best Local Similarity 58.6%; Pred. No. 3.1e-112;
Matches 849; Conservative 0; Mismatches 584; Indels 15; Gaps 4;

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Qy        164 GGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACC 223
              ||||||||  |  ||||    |  |||  |  |||||  |  |||  |      |  |||||   ||||  |
Db        179 GGCTGGACTTTCAGAGATTCCTGACCTTGAACCGGACCTTGCTAGTGGCTGCCCGGGATC 238

Qy        224 ATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAC 283
              |  |||    |  |  |||  |   |   |    |  |     |  ||              |||  ||
Db        239 ACGTTTTCTCCTTCGATCTTCAAGCCGAAGAAGAAGGGGAGGGGCTGGTGCCCAACAAGT 298

Qy        284 TGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGG 343
                  |    |  ||   |||        |||||  ||  |   ||      |    ||||||  |   |  ||
Db        299 ATCTA---ACATGGAGAAGCCAAGATGTGGAGAACTGTGCTGTACGGGGAAAGCTGACGG 355

Qy        344 ATGAGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCT 403
              ||||||||  ||||||  ||||    ||||||  |          ||     |   |   |   |||  ||
Db        356 ATGAGTGCTACAACTATATTCGTGTTCTTGTTCCCTGGGACTCCCAGACGCTCCTTGCCT 415

Qy        404 GTGGAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCAT 463
              |||||||  ||   |  ||||  ||||    |||  |  |  ||||   |||    |  |   ||  |  |
Db        416 GTGGAACGAACTCATTCAGCCCTGTGTGCCGCAGCTATGGGATAACTTCGCTGCAGCAGG 475

Qy        464 TCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTG 523
                ||  ||  |||  |  ||  ||    |||   |||||||  |  ||||||||   ||   |||||||  |
Db        476 AGGGTGAGGAACTGAGTGGGCAGGCTCGATGCCCCTTTGATGCCACCCAGTCCAACGTGG 535

Qy        524 CACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACG 583
              |   |  ||||||||  ||  |   ||  ||||||||||||||    |  ||  ||||   ||||  |||  |
Db        536 CCATCTTTGCAGAGGGCAGCCTGTACTCAGCCACAGCTGCGGATTTCCAGGCCAGTGATG 595

Qy        584 CAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAA 643
              |  ||   |||||  |  ||  |||||         ||   |  ||  ||   |||  ||||  |  ||  ||  |
Db        596 CTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCCACTCCGCTCCGCCAAGTATGACTCCA 655

Qy        644 AATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCT 703
              |  |||  |    |||  |||  |||||||  ||  |||  ||||   |  |||||   ||  |||||||||
Db        656 AGTGGCTCCGAGAGCCACACTTTGTCCAGGCCTTGGAGCATGGAGACCATGTCTACTTCT 715

Qy        704 TCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGG 763
              |||||  |  ||   |  |  ||||||  ||         ||||  |||||     |||  |   |  ||  |
Db        716 TCTTCCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAAGGTGCAGTTCTCCCGCGTAG 775

Qy        764 CTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGT 823
              |  |   ||  |||||    |||  |||||  ||  ||  |    |  |  |  ||||     ||  |||||  |
Db        776 CCCGAGTATGTAAACGTGACATGGGCGGCTCGCCTCGGGCCTTGGACCGCCACTGGACAT 835

Qy        824 CGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACA 883
              |  |||||||||    ||   |  ||||||||  ||  |||||  ||||||   |||  |||||   |
Db        836 CCTTCCTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGGACTCTACTTTCTATTTTGATG 895

Qy        884 TTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGT 943
              ||  |  |||||   |  ||  |       |      |   |  ||  ||    ||  |  ||  |  |      |
Db        896 TTTTACAGGCCTTGACTGGGCCTGTGAACCTGCATGGCCGCTCTGCTCTCTTTGGGGTCT 955

Qy        944 TTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACA 1003
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Db        956 TCACCACCCAGACCAATAGCATCCCTGGCTCTGCCGTCTGCGCCTTCTACCTGGATGAGA 1015

Qy       1004 TTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACAC 1063

Db       1016 TTGAGCGTGGGTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGGATGGGGCCTGGACTC 1075

Qy       1064 CAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCT 1123

Db       1076 CTGTGTCTGAGGACAGAGTTCCCTCACCCAGGCCAGGATCCTGTGCAGGAGTAGGGGGAG 1135

Qy       1124 TAGAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGC 1183

Db       1136 CTGCCTTGTTCTCCTCTTCCCGAGACCTCCCTGATGATGTCCTGACCTTCATCAAGGCTC 1195

Qy       1184 ACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAA 1243

Db       1196 ACCCGCTGCTGGACCCCGCTGTACCACCTGTCACCCATCAGCC---TCTACTCACTCTCA 1252

Qy       1244 TGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATC 1303

Db       1253 CTAGCAGGGCCCTACTGACCCAAGTAGCTGTGGATGGCATGGCTGGTCCCCACAGTAACA 1312

Qy       1304 ACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAG 1363

Db       1313 TCACAGTCATGTTCCTTGGCTCCAATGATGGGACAGTGCTGAAGGTGCTGACCCCAGGTG 1372

Qy       1364 GAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTG 1423

Db       1373 GGCGATCCGG---GGGACCTGAGCCCATCCTCCTGGAAGAGATTGATGCCTACAGCCCTG 1429

Qy       1424 AAAAATGCAGCTATGATGGAGTCG------AAGACAAAAGGATCATGGGCATGCAGCTGG 1477

Db       1430 CCCGGTGCAGTGGGAAGCGGACAGCCCAAACAGCACGACGGATCATAGGGCTGGAGCTGG 1489

Qy       1478 ACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTG 1537

Db       1490 ACACTGAGGGTCACAGGCTTTTTGTGGCTTTTTCTGGCTGTATTGTCTACCTCCCTCTCA 1549

Qy       1538 GCCGGTGTGAACGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATT 1597

Db       1550 GCCGGTGTGCCCGGCATGGGGCCTGTCAGAGGAGCTGTTTGGCTTCTCAGGACCCATACT 1609

Qy       1598 GTGGATGG 1605

Db       1610 GTGGATGG 1617
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RESULT 9
US-09-254-594-4
; Sequence 4, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P

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;  CURRENT APPLICATION NUMBER: US/09/254,594
;  CURRENT FILING DATE:  1999-05-11
;  NUMBER OF SEQ ID NOS: '  13
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 3432
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Tissue Type: Child Brain
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(187)
;   OTHER INFORMATION: Identification Method: E
;   NAME/KEY: misc_feature
;   LOCATION: (188)..(2977)
;   OTHER INFORMATION: CDS; Identification Method: E
;   NAME/KEY: 3'UTR
;   LOCATION: (2978)..(3407)
;   OTHER INFORMATION: Identification Method: E
;   NAME/KEY: polyA_signal
;   LOCATION: (3408)..(3432)
;   OTHER INFORMATION: Identification Method: E
US-09-254-594-4

  Query Match             14.3%;  Score 443.6;  DB 4;  Length 3432;
  Best Local Similarity   58.6%;  Pred. No. 3.5e-112;
  Matches  849;  Conservative    0;  Mismatches  584;  Indels   15;  Gaps    4;

Qy        164 GGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACC 223
              |||||||| | ||||   |  ||| | ||||| | ||| |     | |||||  |||| |
Db        366 GGCTGGACTTTCAGAGATTCCTGACCTTGAACCGGACCTTGCTAGTGGCTGCCCGGGATC 425

Qy        224 ATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAC 283
              |  |||   |  | ||| |  |  |   | |    |  ||            ||| ||
Db        426 ACGTTTTCTCCTTCGATCTTCAAGCCGAAGAAGAAGGGGAGGGGCTGGTGCCCAACAAGT 485

Qy        284 TGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGG 343
                  |   | ||  |||      ||||| || |  ||     |   |||||| |  | ||
Db        486 ATCTA---ACATGGAGAAGCCAAGATGTGGAGAACTGTGCTGTACGGGGAAAGCTGACGG 542

Qy        344 ATGAGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCT 403
              |||||||| |||||| ||||   |||||| |        ||    |  |  |  ||| ||
Db        543 ATGAGTGCTACAACTATATTCGTGTTCTTGTTCCCTGGGACTCCCAGACGCTCCTTGCCT 602

Qy        404 GTGGAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCAT 463
              ||||||| ||  | |||| ||||   ||| | | ||||  |||   | |  || | |
Db        603 GTGGAACGAACTCATTCAGCCCTGTGTGCCGCAGCTATGGGATAACTTCGCTGCAGCAGG 662

Qy        464 TCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTG 523
                || || ||| | || ||   |||  ||||||| | ||||||||  ||  ||||||| |
Db        663 AGGGTGAGGAACTGAGTGGGCAGGCTCGATGCCCCTTTGATGCCACCCAGTCCAACGTGG 722

Qy        524 CACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACG 583
              |  | |||||||| || |  || ||||||||||||   | || ||||  |||| ||| |
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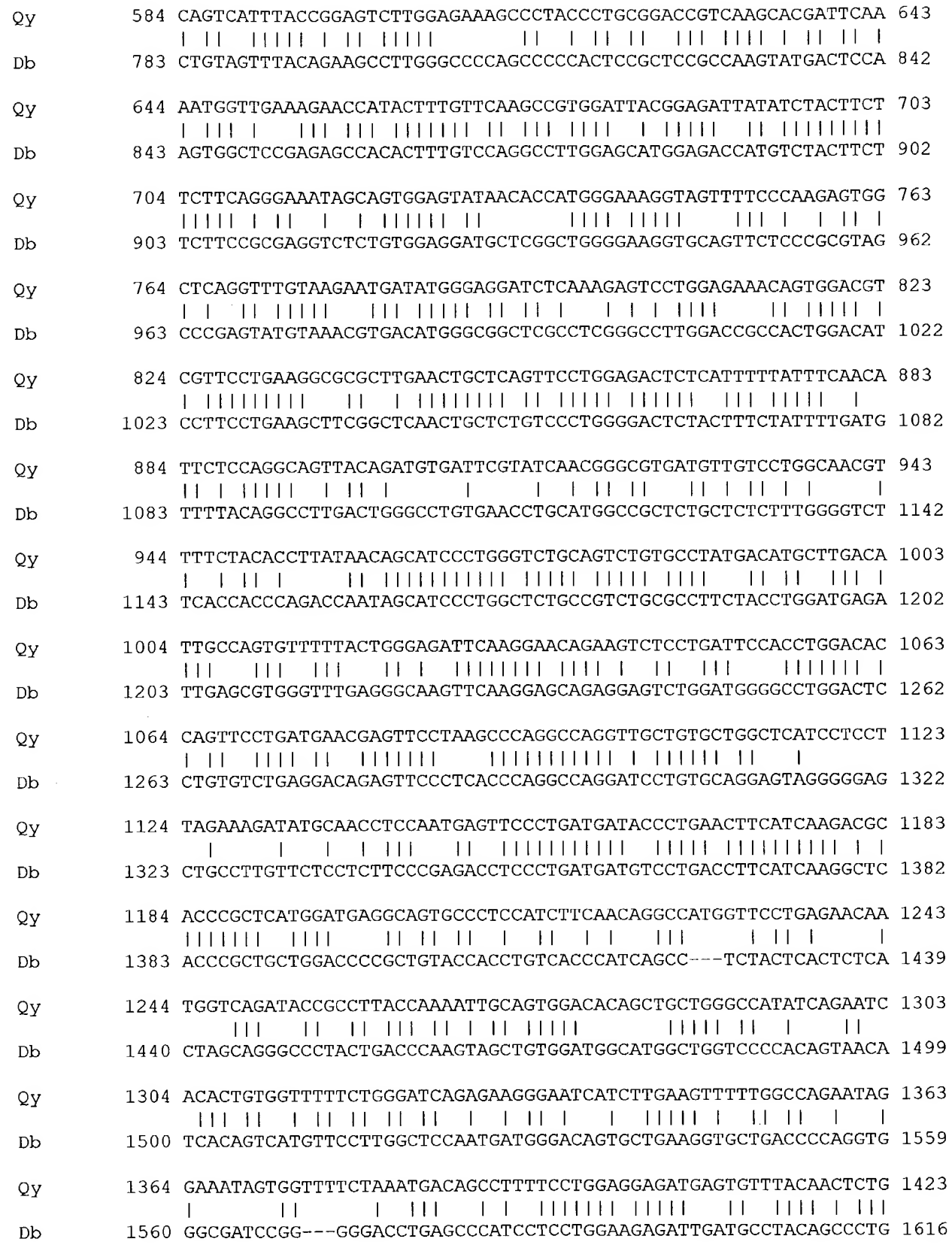

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Qy       1424 AAAAATGCAGCTATGATGGAGTCG------AAGACAAAAGGATCATGGGCATGCAGCTGG 1477
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Db       1617 CCCGGTGCAGTGGGAAGCGGACAGCCCAAACAGCACGACGGATCATAGGGCTGGAGCTGG 1676

Qy       1478 ACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTG 1537
              |||  |   |   |   || | ||| || || |||  |||| |  |  |  | || ||
Db       1677 ACACTGAGGGTCACAGGCTTTTTGTGGCTTTTTCTGGCTGTATTGTCTACCTCCCTCTCA 1736

Qy       1538 GCCGGTGTGAACGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATT 1597
              |||||||||  || ||||||   ||| | |  | |||| | || ||    |||||||| |
Db       1737 GCCGGTGTGCCCGGCATGGGGCCTGTCAGAGGAGCTGTTTGGCTTCTCAGGACCCATACT 1796

Qy       1598 GTGGATGG 1605
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Db       1797 GTGGATGG 1804
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RESULT 10
US-09-254-594-2
; Sequence 2, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Tissue Type: Brain
; NAME/KEY: CDS
; LOCATION: (1)..(2787)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-2

  Query Match 12.0%; Score 369.8; DB 4; Length 2787;
  Best Local Similarity 55.9%; Pred. No. 7.8e-92;
  Matches 811; Conservative 0; Mismatches 622; Indels 18; Gaps 5;

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Qy        164 GGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACC 223
              |||||||| | ||||   |  ||| | ||||| | ||| |     | |||||  |||| |
Db        176 GGCTGGACTTTCAGAGATTCCTGACCTTGAACCGGACCTTGCTTGTGGCTGCCCGGGATC 235

Qy        224 ATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAC 283
              |  |||   |  | ||| |  |  |   | |    |  ||           ||| ||
Db        236 ACGTTTTCTCCTTCGATCTTCAAGCCCAAGAAGAAGGGGAGGGGCTGGTGCCCAACAAGT 295
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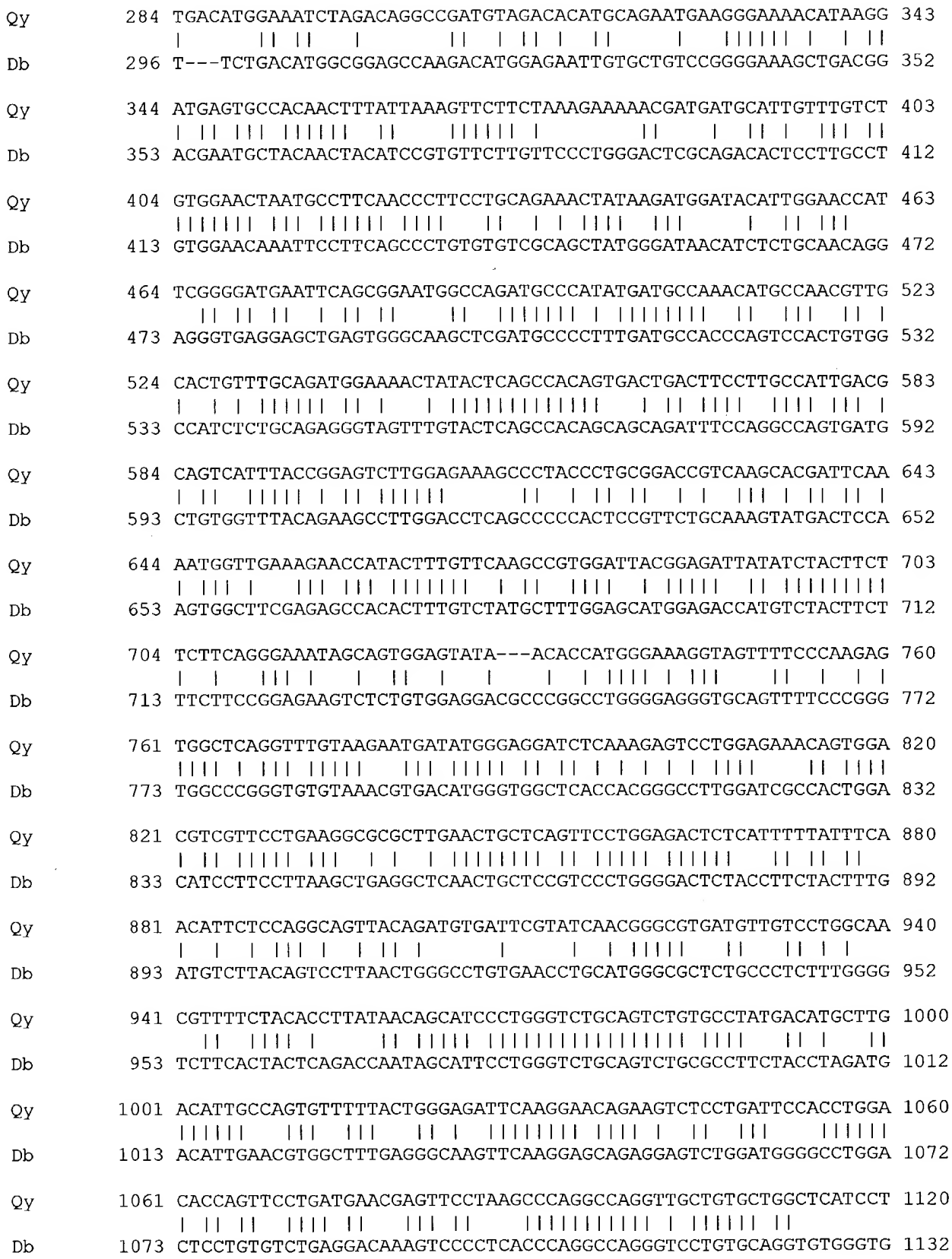

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Qy       1121 CCTTAGAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGA 1180
Db       1133 CAGCTGCCTTATTCTCCTCCTCTCAAGACCTGCCTGACGATGTCCTGCTCTTCATCAAGG 1192

Qy       1181 CGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAA 1240
Db       1193 CACACCCACTGCTGGATCCCGCTGTGCCACC---TGCCACCCATCAACCTCTCCTCACTC 1249

Qy       1241 CAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGA 1300
Db       1250 TGACTAGCAGGGCTCTACTGACCCAGGTAGCTGTGGATGGTATGGCTGGCCCCCACAGAA 1309

Qy       1301 ATCACACTGTGGTTTTTCTGGGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAA 1360
Db       1310 ATACTACAGTCCTGTTTCTTGGCTCCAATGATGGGACAGTGCTGAAGGTGCTACCTCCAG 1369

Qy       1361 TAGGAAATAGTGGTTTTCTAAATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACT 1420
Db       1370 GGGGACA---GTCTCTGGGACCCGAGCCTATCATATTGGAAGAGATTGATGCCTACAGCC 1426

Qy       1421 CTGAAAAATGCAGCTATGATGG------AGTCGAAGACAAAAGGATCATGGGCATGCAGC 1474
Db       1427 ATGCCCGGTGCAGTGGGAAGCGGTCACCCCGAGCTGCTCGACGGATCATAGGGCTGGAGC 1486

Qy       1475 TGGACAGAGCAAGCAGCTCTCTGTATGTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCC 1534
Db       1487 TGGACACTGAGGGTCACAGGCTTTTTGTGGCCTTTCCTGGATGCATCGTCTACCTCTCTC 1546

Qy       1535 TTGGCCGGTGTGAACGACATGGGAAGTGTAAAAAAACCTGTATTGCCTCCAGAGACCCAT 1594
Db       1547 TCAGCCGCTGTGCCCGGCATGGAGCATGTCAGAGGAGCTGCCTGGCTTCTCTGGACCCAT 1606

Qy       1595 ATTGTGGATGG 1605
Db       1607 ACTGTGGATGG 1617
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RESULT 11
US-09-254-594-1
; Sequence 1, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
;  APPLICANT:  KIMURA, Toru
;  APPLICANT:  KIKUCHI, Kaoru
;  TITLE OF INVENTION:   NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
;  FILE REFERENCE:   0020-4527P
;  CURRENT APPLICATION NUMBER: US/09/254,594
;  CURRENT FILING DATE:  1999-05-11
;  NUMBER OF SEQ ID NOS:   13
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 3195
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
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; OTHER INFORMATION: Tissue Type: Brain
; NAME/KEY: 5'UTR
; LOCATION: (1)..(50)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: misc_feature
; LOCATION: (51)..(2837)
; OTHER INFORMATION: CDS; Identification Method: E
; NAME/KEY: 3'UTR
; LOCATION: (2838)..(3195)
; OTHER INFORMATION: Identification Method: E
US-09-254-594-1

Query Match 12.0%; Score 369.8; DB 4; Length 3195;
Best Local Similarity 55.9%; Pred. No. 8.5e-92;
Matches 811; Conservative 0; Mismatches 622; Indels 18; Gaps 5;

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Qy        164 GGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACC 223
              ||||||| | ||||  |  ||| | ||||| | ||| |     | |||||  |||| |
Db        226 GGCTGGACTTTCAGAGATTCCTGACCTTGAACCGGACCTTGCTTGTGGCTGCCCGGGATC 285

Qy        224 ATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAC 283
              |  |||   |  | |||  |  |  |  | |    |  ||             ||| ||
Db        286 ACGTTTTCTCCTTCGATCTTCAAGCCCAAGAAGAAGGGGAGGGGCTGGTGCCCAACAAGT 345

Qy        284 TGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGG 343
              |      || ||   |       ||  | || |  ||     |   |||||| |  | ||
Db        346 T---TCTGACATGGCGGAGCCAAGACATGGAGAATTGTGCTGTCCGGGGAAAGCTGACGG 402

Qy        344 ATGAGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCT 403
              | || ||| ||||||  ||    |||||| |         ||    |  || |  ||| ||
Db        403 ACGAATGCTACAACTACATCCGTGTTCTTGTTCCCTGGGACTCGCAGACACTCCTTGCCT 462

Qy        404 GTGGAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCAT 463
              ||||||| ||| |||||| ||||   ||  | | ||||  |||     |  || |||
Db        463 GTGGAACAAATTCCTTCAGCCCTGTGTGTCGCAGCTATGGGATAACATCTCTGCAACAGG 522

Qy        464 TCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTG 523
                || || ||  | || ||    ||  ||||||| | ||||||||  ||  |||  || |
Db        523 AGGGTGAGGAGCTGAGTGGGCAAGCTCGATGCCCCTTTGATGCCACCCAGTCCACTGTGG 582

Qy        524 CACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACG 583
              |  | | |||||| || |   | ||||||||||||||   | || ||||  |||| ||| |
Db        583 CCATCTCTGCAGAGGGTAGTTTGTACTCAGCCACAGCAGCAGATTTCCAGGCCAGTGATG 642

Qy        584 CAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAA 643
              | ||  ||||| | || ||||||      ||  | || ||  | |  ||| | || || |
Db        643 CTGTGGTTTACAGAAGCCTTGGACCTCAGCCCCCACTCCGTTCTGCAAAGTATGACTCCA 702

Qy        644 AATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCT 703
              | ||| |   ||| ||| |||||||  | ||  ||||  | |||||  || |||||||||
Db        703 AGTGGCTTCGAGAGCCACACTTTGTCTATGCTTTGGAGCATGGAGACCATGTCTACTTCT 762

Qy        704 TCTTCAGGGAAATAGCAGTGGAGTATA---ACACCATGGGAAAGGTAGTTTTCCCAAGAG 760
              |  |   ||| |   |  ||  |   |    |  | |||| | |||    ||  |  | |
Db        763 TTCTTCCGGAGAAGTCTCTGTGGAGGACGCCCGGCCTGGGGAGGGTGCAGTTTTCCCGGG 822

Qy        761 TGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGA 820
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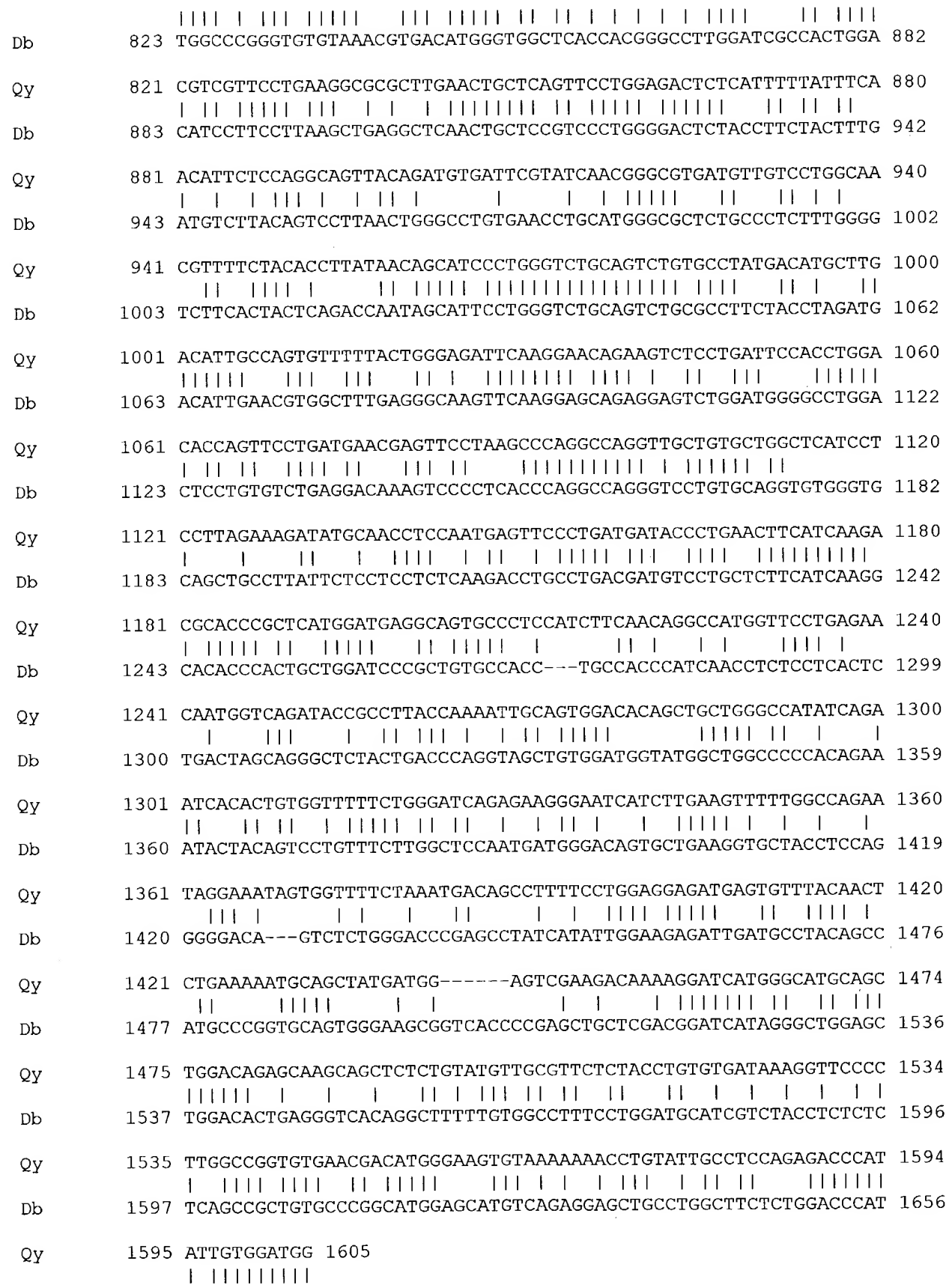

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Db        1657 ACTGTGGATGG 1667


RESULT 12
US-09-833-381-112
; Sequence 112, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
;  FILE REFERENCE: 5800-119
;  CURRENT APPLICATION NUMBER: US/09/833,381
;  CURRENT FILING DATE:  2001-04-11
;  PRIOR APPLICATION NUMBER: 09/516,448
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 2050
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 112
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(591)
;   OTHER INFORMATION: n = A,T,C or G
US-09-833-381-112

  Query Match             11.9%;  Score 368;  DB 4;  Length 591;
  Best Local Similarity   90.2%;  Pred. No. 1e-91;
  Matches  415;  Conservative    0;  Mismatches   42;  Indels    3;  Gaps    2;

Qy       1832 ACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGA 1891
              ||| |  | |||   |     |    || |  |  | | | |||   |     |    ||
Db        132 ACTTAAGTCACAATCCTTTGTCAGGAGGAGGGGCATTTCCACATTCCCTTGTTGCACTGA 191

Qy       1892 AGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCT 1951
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 ATGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCT 251

Qy       1952 TGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCT 2011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 TGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCT 311

Qy       2012 ACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGC 2071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 ACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGC 371

Qy       2072 TCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGG 2131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 TCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGG 431

Qy       2132 ACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCA 2191
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        432 ACACTCAATCCAAAGACCCAAAGCCGGAGGCATTCCTCACGCCACTCATGCACAACGGCA 491

Qy       2192 AGCTCGCCACT--CCCGGCAACACGGCCAAGATGCTCA-TTAAAGCAGACCAGCACCACC 2248
              ||||||||||||  || |||||||||||||||||||| ||||||||||||||| ||||
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Db        492 AGCTCGCCACTTCCCGGGCAACACGGCCAAGATGCTCATTTAAAGCAGACCAGCANCACC 551

Qy       2249 TGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAAC 2288
              ||||||||| ||||||||||||||||||||||||||||||
Db        552 TGGACCTGANGGCCCTCCCCACCCCAGAGTCAACCCCAAC 591
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RESULT 13
US-09-976-594-632
; Sequence 632, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 632
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 238322.6
US-09-976-594-632

Query Match 8.2%; Score 252.6; DB 4; Length 4286;
Best Local Similarity 58.9%; Pred. No. 2.6e-59;
Matches 472; Conservative 0; Mismatches 324; Indels 5; Gaps 2;

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Qy        164 GGCTGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACC 223
              |||||||| | ||||   |  ||| | ||||| | ||| |     | |||||  |||| |
Db        431 GGCTGGACTTTCAGAGATTCCTGACCTTGAACCGGACCTTGCTAGTGGCTGCCCGGGATC 490

Qy        224 ATATTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAAC 283
              |  |||   |  | ||| |  |  |   | |    |  ||           ||| ||
Db        491 ACGTTTTCTCCTTCGATCTTCAAGCCGAAGAAGAAGGGGAGGGGCTGGTGCCCAACAA-- 548

Qy        284 TGACATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGG 343
               |      | ||  |||      ||||| || |  ||     |   |||||| |  | ||
Db        549 -GTATCTAACATGGAGAAGCCAAGATGTGGAGAACTGTGCTGTACGGGGAAAGCTGACGG 607

Qy        344 ATGAGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCT 403
              |||||||| |||||| ||||   |||||| |        ||    |  |  |  ||| ||
Db        608 ATGAGTGCTACAACTATATTCGTGTTCTTGTTCCCTGGGACTCCCAGACGCTCCTTGCCT 667

Qy        404 GTGGAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCAT 463
              |||||||  ||  | ||||  ||||   |||  | | ||||  |||   | |  || | |
Db        668 GTGGAACGAACTCATTCAGCCCTGTGTGCCGCAGCTATGGGATAACTTCGCTGCAGCAGG 727

Qy        464 TCGGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTG 523
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                 || || ||| | || ||   |||  ||||||| | ||||||||  ||  ||||||| |
Db        728 AGGGTGAGGAACTGAGTGGGCAGGCTCGATGCCCCTTTGATGCCACCCAGTCCAACGTGG 787

Qy        524 CACTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACG 583
              |  | |||||||| || |  || ||||||||||||   | || ||||  |||| ||| |
Db        788 CCATCTTTGCAGAGGGCAGCCTGTACTCAGCCACAGCTGCGGATTTCCAGGCCAGTGATG 847

Qy        584 CAGTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAA 643
              | ||  ||||| | || |||||       ||  | || ||  ||| |||| | || || |
Db        848 CTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCCACTCCGCTCCGCCAAGTATGACTCCA 907

Qy        644 AATGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCT 703
              | ||| |   ||| ||| ||||||| || ||| ||||  | |||||  || |||||||||
Db        908 AGTGGCTCCGAGAGCCACACTTTGTCCAGGCCTTGGAGCATGGAGACCATGTCTACTTCT 967

Qy        704 TCTTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGG 763
              ||||| | ||  |  | |||||| ||       |||| | |||    ||| |  | || |
Db        968 TCTTCCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAGGGTGCAGTTCTCCCGCGTAG 1027

Qy        764 CTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCT--GGAGAAACAGTGGAC 821
              | |  || |||||   ||| ||||| || || |    |  ||  | |    || |||||
Db       1028 CCCGAGTATGTAAACGTGACATGGGCGGCTCGCCTTCGGGTCTTGGTACCGCCACTGGAC 1087

Qy        822 GTCGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAA 881
               || |||||||||   ||  | |||||||| || ||||| ||||||  ||| |||||  |
Db       1088 ATCCTTCCTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGGACTCTACTTTCTATTTTGA 1147

Qy        882 CATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAAC 941
               || | |||||  | || | .     |     |  | || ||   || | || | |
Db       1148 TGTTTTACAGGCCTTGACTGGGCCTGTGAACCTGCATGGCCGCTCTGCTCTCTTTGGGGT 1207

Qy        942 GTTTTCTACACCTTATAACAG 962
               ||  | || |     || ||
Db       1208 CTTCACCACCCAGACCAATAG 1228
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RESULT 14
US-09-833-381-3
; Sequence 3, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
;  FILE REFERENCE: 5800-119
;  CURRENT APPLICATION NUMBER: US/09/833,381
;  CURRENT FILING DATE:  2001-04-11
;  PRIOR APPLICATION NUMBER: 09/516,448
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 2050
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 775
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(775)
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; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-3

Query Match 7.1%; Score 220; DB 4; Length 775;
Best Local Similarity 100.0%; Pred. No. 9.8e-51;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        743 AGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAG 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 AGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAG 190

Qy        803 TCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAG 862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 TCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAG 250

Qy        863 ACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGC 922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 ACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGC 310

Qy        923 GTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAACAG 962
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Db        311 GTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAACAG 350
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RESULT 15
US-08-121-713D-57
; Sequence 57, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
;   APPLICANT: Goodman, Corey S.
;   APPLICANT: Kolodkin, Alex L.
;   APPLICANT: Matthes, David
;   APPLICANT: Bentley, David R.
;   APPLICANT: O'Connor, Timothy
;   TITLE OF INVENTION: The Semaphorin Gene Family
;   NUMBER OF SEQUENCES: 100
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;   STREET: 268 Bush Street, Suite 3200
;   CITY: San Francisco
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94104
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/121,713D
;   FILING DATE: 13-SEP-1993
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Osman, Richard A.
;   REGISTRATION NUMBER: 36,627
;   REFERENCE/DOCKET NUMBER: B94-002-1
;   TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 451..2640
US-08-121-713D-57

Query Match 5.4%; Score 166; DB 1; Length 2854;
Best Local Similarity 53.0%; Pred. No. 1.8e-35;
Matches 532; Conservative 0; Mismatches 415; Indels 57; Gaps 6;

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Qy        289 TGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAG 348
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Db        709 TGGCACTCGTCAGGTGCCCATCGCGAGCTCTGCTACCTCAAGGGGAAGTCAGAGGACGAC 768

Qy        349 TGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGA 408
              ||||| ||||  ||   ||| ||    || |   |||||||     |  |  |||| ||
Db        769 TGCCAGAACTACATCCGAGTCCTGGCGAAAATTGACGATGACCGCGTACTCATCTGCGGT 828

Qy        409 ACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGAT---GGATACATTGGAACCATTC 465
              || || ||||  || ||    ||  |  ||||     |   ||||  |    |     |
Db        829 ACGAACGCCTATAAGCCACTATGTCGGCACTACGCCCTCAAGGATGGAGATTATGTTGTA 888

Qy        466 GGGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCA 525
              | | | ||||     ||||  |     ||||||| |||  |  | ||   || |  ||||
Db        889 GAGAAAGAATATGAGGGAAGAGGATTGTGCCCATTTGACCCTGACCACAACAGCACTGCA 948

Qy        526 CTGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCA 585
               | |     || ||| || | |||||||| |||||| | ||||||  ||  | |||| |
Db        949 ATATACAGTGAGGGACAATTGTACTCAGCAACAGTGGCAGACTTCTCTGGAACTGACCCT 1008

Qy        586 GTCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAA 645
               |||| |||||  | |               | ||  | || |  |     ||   |||
Db       1009 CTCATATACCGCGGCC---------------CTCTAAGAACAGAGAGATCTGACCTCAAA 1053

Qy        646 TGGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTC 705
                || || |  ||  |||||||  |  |  |||| |||   |||| ||| | |||||||
Db       1054 CAATTAAATGCTCCTAACTTTGTCAACACAATGGAGTACAATGATTTTATATTCTTCTTC 1113

Qy        706 TTCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCT 765
              ||| | || |  || || ||||| | || |   |||||||   | |   ||||||| ||
Db       1114 TTCCGAGAGACTGCTGTTGAGTACATCAACTGCGGAAAGGCTATCTATTCAAGAGTTGCC 1173

Qy        766 CAGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCG 825
                || |||||  |||| | ||| ||  ||||    |     || | |   ||||| ||
Db       1174 AGAGTCTGTAAACATGACAAGGGCGGCCCTCATCAGGGTGGTGACAGA---TGGACTTCT 1230

Qy        826 TTCCTGAAGGCGCGCTTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATT 885
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Db       1231 TTTTTGAAATCACGTCTGAACTGTTCCGTCCCTGGAGATTATCCATTTTACTTCAATGAA 1290

Qy        886 CTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAAC---- 941
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Db       1291 ATTCAGTCAACAAGTGACATCATTGAAGGAAATTATGGTGGTCAAGTGGAGAAACTCATC 1350

Qy        942 --------GTTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGAC 993
                      ||  | |||||    |||   ||   ||| ||||| || |||||||
Db       1351 TACGGTGTCTTCACGACACCAGTGAACTCTATTGGTGGCTCTGCTGTTTGTGCCTTCAGT 1410

Qy        994 ATGCTTGACATTGCCAGTGTTTTTACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCC 1053
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Db       1411 ATGAAGTCAATACTTGAGTCATTTGATGGTCCATTTAAAGAGCAGGAAACGATGAACTCA 1470

Qy       1054 ACCTGGACACCAGTTCCTGATGAACGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGC 1113
              | ||||    ||||  ||         |||  ||  | || |||||  ||    ||||
Db       1471 AACTGGTTGGCAGTGCCAAGCCTTAAAGTGCCAGAACCAAGGCCTGGACAATGTGT---- 1526

Qy       1114 TCATCCTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCCTGATGATACCCTGAACTTC 1173
                        ||| || |  |   | |        | |||||||   |  | || ||
Db       1527 ------------GAATGACAGTCGTACAC--------TTCCTGATGTGTCTGTCAATTTT 1566

Qy       1174 ATCAAGACGCACCCGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTC 1233
              | ||| | ||  | || ||||||||||| |||||  |  | || |   |||||    ||
Db       1567 GTAAAGTCACATACACTGATGGATGAGGCCGTGCCAGCATTTTTTACTCGGCCAATTCTC 1626

Qy       1234 CTGAGAACAATGGTCAGATACCGCCTTACCAAAATTGCAGTGGA 1277
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Db       1627 ATTCGGATCAGCTTACAGTACAGATTTACAAAAATAGCTGTTGA 1670
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Job time : 229.203 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 25, 2004, 23:27:11 ; Search time 1097.37 Seconds
(without alignments)
10493.560 Million cell updates/sec

Title: US-09-856-681A-1
Perfect score: 3093
Sequence: 1 atgaggtcagaagccttgct.....ccaatgatgcgtgtacataa 3093

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2458946 seqs, 1861504846 residues

Total number of hits satisfying chosen parameters: 4917892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	3038	98.2	3498	10	US-09-991-053-3	Sequence 3, Appli
2	3038	98.2	3498	10	US-09-957-187-3	Sequence 3, Appli
3	3038	98.2	3498	12	US-10-403-676-31	Sequence 31, Appl
4	3038	98.2	3498	15	US-10-449-548-31	Sequence 31, Appl
5	3037.6	98.2	3055	12	US-10-403-676-27	Sequence 27, Appl
6	3037.6	98.2	3055	15	US-10-449-548-27	Sequence 27, Appl
7	3032	98.0	4250	14	US-10-393-892-30	Sequence 30, Appl
8	3032	98.0	4250	14	US-10-394-382-30	Sequence 30, Appl
9	3032	98.0	4280	15	US-10-120-988-330	Sequence 330, App
10	3030.4	98.0	4250	10	US-09-957-187-84	Sequence 84, Appl
11	3030.4	98.0	4250	12	US-10-403-676-13	Sequence 13, Appl
12	3030.4	98.0	4250	15	US-10-449-548-13	Sequence 13, Appl
13	3025.8	97.8	3165	12	US-10-403-676-47	Sequence 47, Appl
14	3025.8	97.8	3165	15	US-10-449-548-47	Sequence 47, Appl
15	2975	96.2	3106	12	US-10-403-676-17	Sequence 17, Appl
16	2975	96.2	3106	15	US-10-449-548-17	Sequence 17, Appl
17	2860.8	92.5	2995	12	US-10-403-676-19	Sequence 19, Appl
18	2860.8	92.5	2995	15	US-10-449-548-19	Sequence 19, Appl
19	2746.8	88.8	2944	12	US-10-403-676-29	Sequence 29, Appl
20	2746.8	88.8	2944	15	US-10-449-548-29	Sequence 29, Appl
21	2727.4	88.2	3983	12	US-10-403-676-45	Sequence 45, Appl
22	2727.4	88.2	3983	15	US-10-449-548-45	Sequence 45, Appl
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26	1881.6	60.8	1890	10	US-09-957-187-29	Sequence 29, Appl
27	1881.6	60.8	1890	10	US-09-957-187-82	Sequence 82, Appl
28	1879.2	60.8	2583	12	US-10-403-676-51	Sequence 51, Appl
29	1879.2	60.8	2583	15	US-10-449-548-51	Sequence 51, Appl
30	1878	60.7	1878	12	US-10-403-676-33	Sequence 33, Appl
31	1878	60.7	1878	15	US-10-449-548-33	Sequence 33, Appl
32	1816.2	58.7	1948	12	US-10-403-676-49	Sequence 49, Appl
33	1816.2	58.7	1948	15	US-10-449-548-49	Sequence 49, Appl
34	1815.4	58.7	2113	12	US-10-403-676-55	Sequence 55, Appl
35	1815.4	58.7	2113	15	US-10-449-548-55	Sequence 55, Appl
36	1815	58.7	2634	12	US-10-403-676-53	Sequence 53, Appl
37	1815	58.7	2634	15	US-10-449-548-53	Sequence 53, Appl
38	1788.6	57.8	1921	12	US-10-403-676-15	Sequence 15, Appl
39	1788.6	57.8	1921	15	US-10-449-548-15	Sequence 15, Appl
40	1719.4	55.6	1908	12	US-10-403-676-35	Sequence 35, Appl
41	1719.4	55.6	1908	15	US-10-449-548-35	Sequence 35, Appl
42	1476.2	47.7	1492	12	US-10-403-676-23	Sequence 23, Appl
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ALIGNMENTS

RESULT 1
US-09-991-053-3
; Sequence 3, Application US/09991053
; Publication No. US20030003532A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.

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;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
;  TITLE OF INVENTION:  MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
;  FILE REFERENCE: 15966-540 CON S-10
;  CURRENT APPLICATION NUMBER: US/09/991,053
;  CURRENT FILING DATE:  2002-05-23
;  PRIOR APPLICATION NUMBER: USSN 60/123,667
;  PRIOR FILING DATE: 1999-03-09
;  PRIOR APPLICATION NUMBER: 09/520,781
;  PRIOR FILING DATE: 2000-03-08
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3498
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (214)..(3030)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (3047)
;   OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-991-053-3

  Query Match             98.2%;  Score 3038;  DB 10;  Length 3498;
  Best Local Similarity   99.3%;  Pred. No. 0;
  Matches 3072;  Conservative    0;  Mismatches   21;  Indels    2;  Gaps    2;

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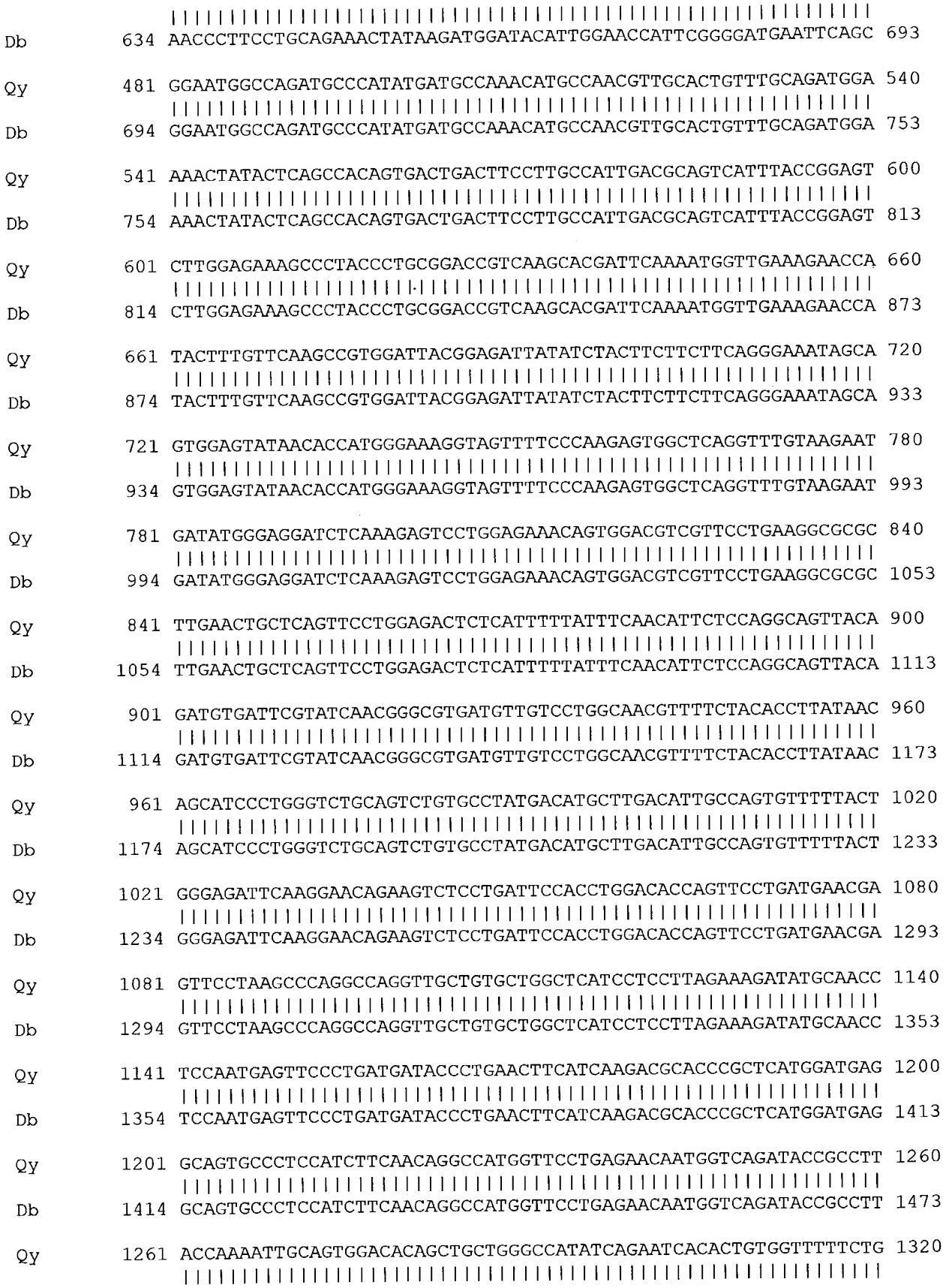

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Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Qy       2281 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC 2340
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Db       2854 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2913

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RESULT 2
US-09-957-187-3
; Sequence 3, Application US/09957187
; Publication No. US20030054514A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard A.
;  APPLICANT:  LaRochelle, William
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
;  FILE REFERENCE: 15966-540 CIP
;  CURRENT APPLICATION NUMBER: US/09/957,187
;  CURRENT FILING DATE:  2000-09-19
;  PRIOR APPLICATION NUMBER: 60/123,667
;  PRIOR FILING DATE: 1999-03-09
;  PRIOR APPLICATION NUMBER: 09/520,781
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/234,082
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: 60/233,798
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 60/174,485
;  PRIOR FILING DATE: 2000-01-04
;  NUMBER OF SEQ ID NOS: 85
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;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (214)..(3030)
;   NAME/KEY: misc_feature
;   LOCATION: (3047)
;   OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-957-187-3

  Query Match             98.2%;  Score 3038;  DB 10;  Length 3498;
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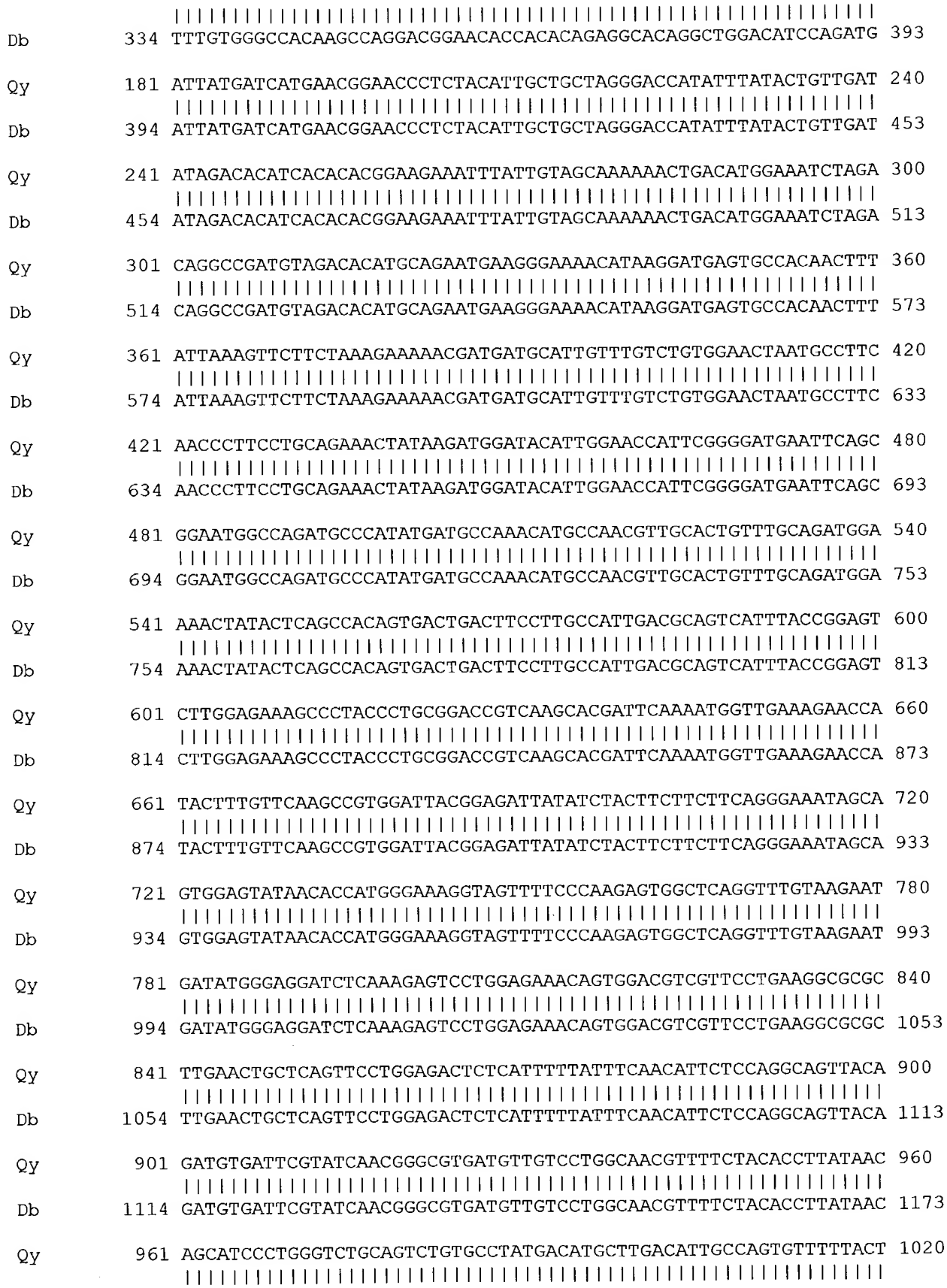

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Qy       2401 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2460
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Db       2614 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2673

Qy       2461 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2733

Qy       2521 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2793

Qy       2581 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2853

Qy       2641 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2913
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Qy       2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2973

Qy       2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAAGAAACAACACTAA 2819
             |||||||||||||||||||||||||| | ||||| ||||||| |||| |||||||||
Db       2974 CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA 3033

Qy       2820 CTCCTCCAATTCCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC 2878
             | ||  |||||| |||  ||   ||  ||||||||||||||||||||||||||||||
Db       3034 CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC 3093

Qy       2879 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 2938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 3153

Qy       2939 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 2998
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Db       3154 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 3213

Qy       2999 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3058
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Db       3214 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3273

Qy       3059 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
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Db       3274 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3308
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RESULT 3
US-10-403-676-31
; Sequence 31, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel

; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 31
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (214)..(3030)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3047)..(3047)
; OTHER INFORMATION: Wherein n may be a, c, g or t
US-10-403-676-31

Query Match 98.2%; Score 3038; DB 12; Length 3498;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 3072; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 273

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        274 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 333

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 393

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 453

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 513

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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Db        514 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 573

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 633

Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 693

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 753

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 813

Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 873

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 933

Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 993

Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1053

Qy        841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1113

Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
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Db       1114 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1173
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Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1233

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1293

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1353

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1413

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
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Db       1414 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1473

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1474 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1533

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1593

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Db       1594 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1653

Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1713

Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1773

Qy       1561 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
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Db       1774 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1833

Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
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Db       1834 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1893

Qy       1681 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGGGCATTCCAGT 1953

Qy       1741 TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1954 TCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGG 2013
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Qy       1801 GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2014 GGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGG 2073

Qy       1861 GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2074 GCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAA 2133

Qy       1921 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2134 GGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTC 2193

Qy       1981 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2194 ATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGAC 2253

Qy       2041 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2254 GTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGC 2313

Qy       2101 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2160
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Db       2314 AGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2373

Qy       2161 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2220
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Db       2374 GCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAG 2433

Qy       2221 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 ATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCA 2493

Qy       2281 ACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAAC 2340
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Db       2554 CAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCC 2613

Qy       2401 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2460
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Db       2614 ACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATC 2673

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Db       2674 ACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAG 2733

Qy       2521 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2580
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Db       2734 ATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGC 2793

Qy       2581 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2640
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Db       2794 AGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAA 2853

Qy       2641 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2700
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Db       2854 GTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTA 2913

Qy       2701 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2760
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 AGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTAC 2973

Qy       2761 CCCACGAACTCGCTCACGAGAAGCCACCAGGCCACC-ACTCTCAAAAGAAACAACACTAA 2819
                |||||||||||||||||||||||||| | ||||| |||||||  |||| |||||||||
Db       2974 CCCACGAACTCGCTCACGAGAAGCCACCTGACCACCTACTCTCATCAGAAGCAACACTAA 3033

Qy       2820 CTCCTCCAATTCCTCTC-ACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGC 2878
                | ||  ||||||  |||   ||    ||  ||||||||||||||||||||||||||||||
Db       3034 CCCCGACAATTCANCTCTGACTTCAAAGGGACCAGAGCTTTGGCAGGGGAGACAACCCGC 3093

Qy       2879 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 2938
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 CGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGG 3153

Qy       2939 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 2998
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 CCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGC 3213

Qy       2999 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3058
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Db       3214 TGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTT 3273

Qy       3059 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3093
                |||||||||||||||||||||||||||||||||
Db       3274 CCACATCCATGAAGCCCAATGATGCGTGTACATAA 3308
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RESULT 4
US-10-449-548-31
; Sequence 31, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082

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;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: 60/233,798
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 60/174,485
;  PRIOR FILING DATE: 2000-01-04
;  PRIOR APPLICATION NUMBER: 10/403,676
;  PRIOR FILING DATE: 2003-03-31
;  PRIOR APPLICATION NUMBER: 60/371,002
;  PRIOR FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: 60/384,798
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: 60/402,407
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: 60/443,062
;  PRIOR FILING DATE: 2003-01-28
;  NUMBER OF SEQ ID NOS: 58
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; SEQ ID NO 31
;   LENGTH: 3498
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
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;   LOCATION: (3047)..(3047)
;   OTHER INFORMATION: Wherein n may be a, c, g or t
US-10-449-548-31

  Query Match             98.2%;  Score 3038;  DB 15;  Length 3498;
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Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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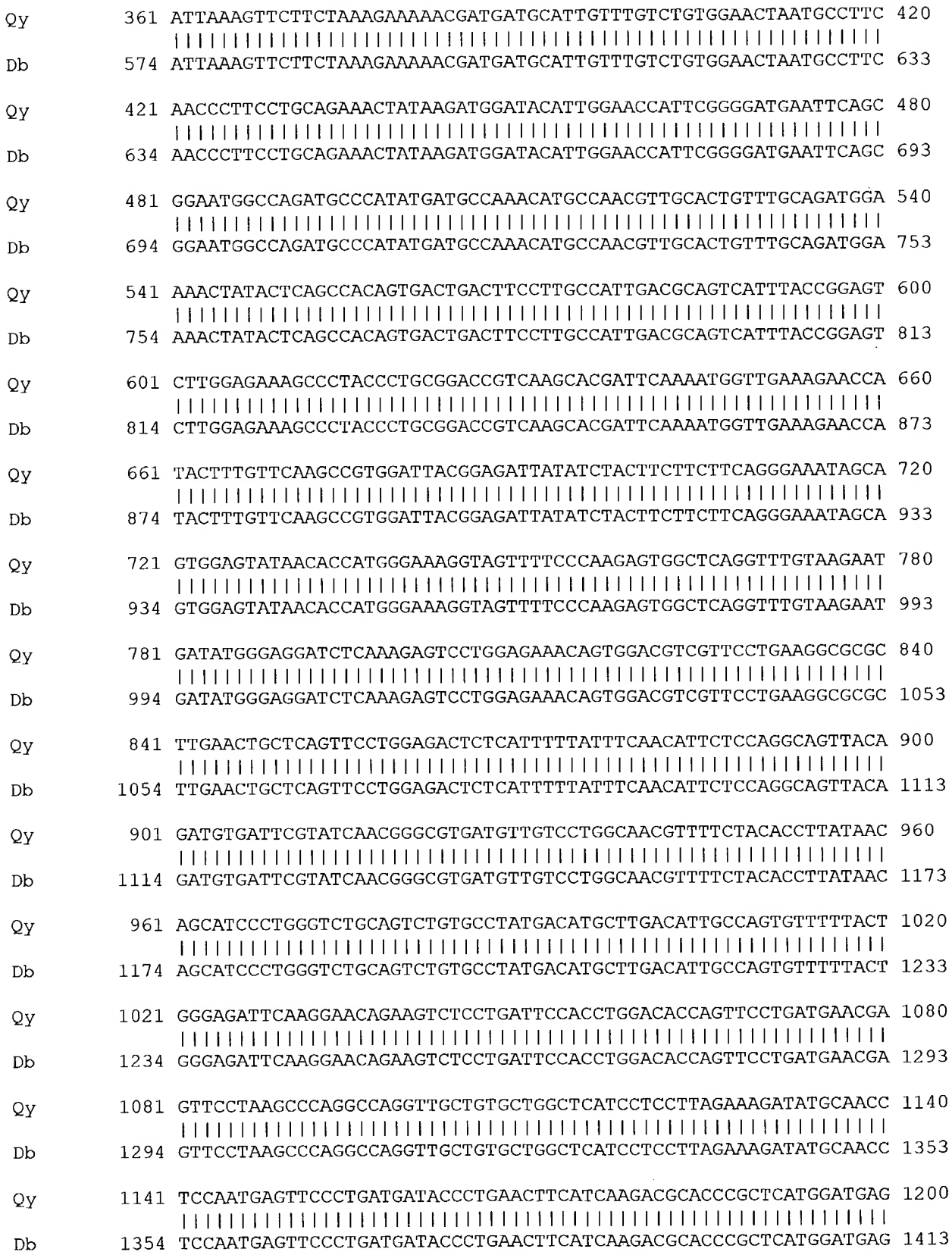

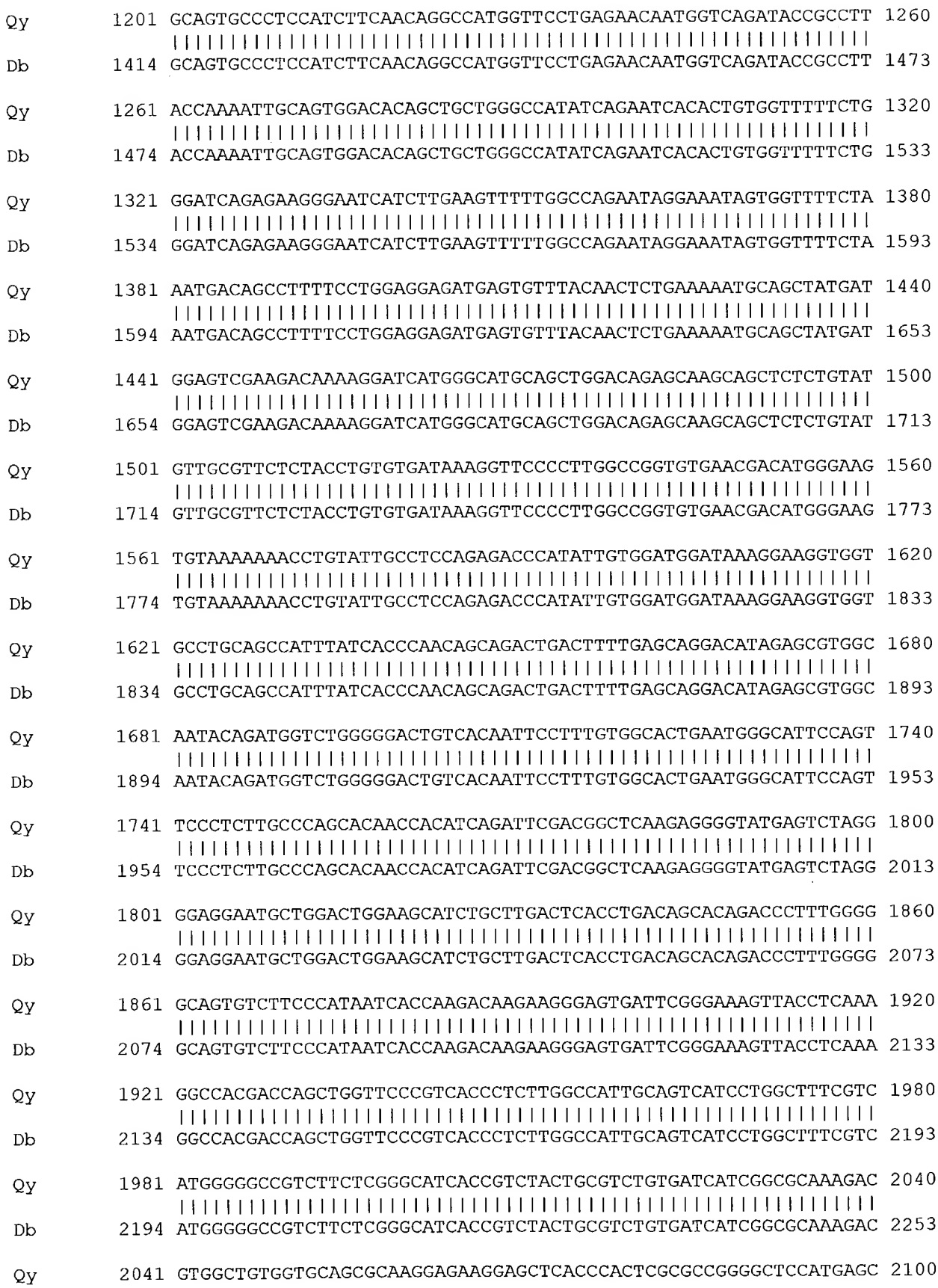
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Db 1414 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1473
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Db 1474 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1533
Qy 1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
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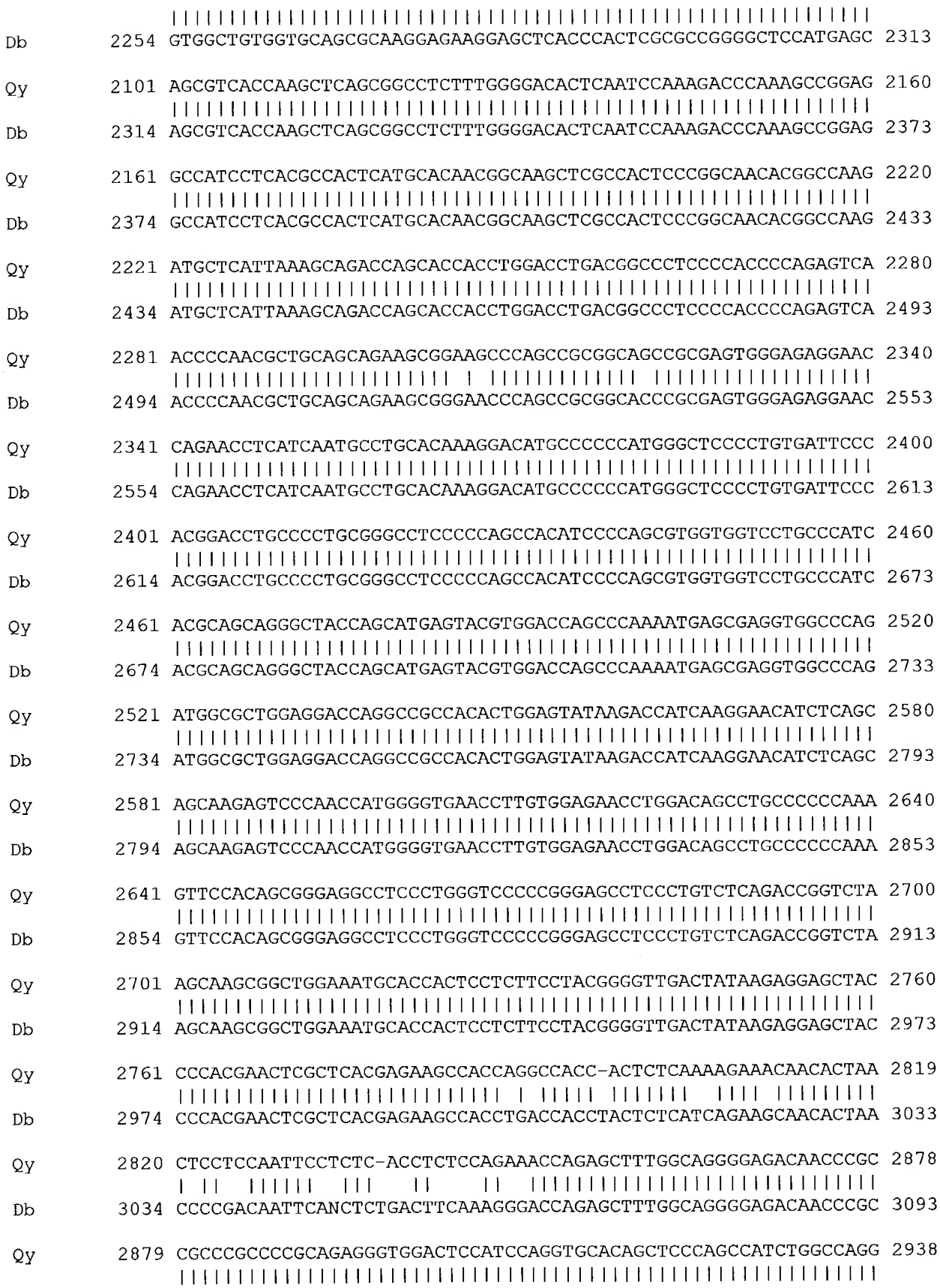

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RESULT 5
US-10-403-676-27
; Sequence 27, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781

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;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 09/957,187
;  PRIOR FILING DATE: 2001-09-19
;  PRIOR APPLICATION NUMBER: 60/371,002
;  PRIOR FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 09/538,092
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: 09/604,286
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/140,584
;  PRIOR FILING DATE: 1999-06-23
;  PRIOR APPLICATION NUMBER: 60/370,381
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: 60/384,297
;  PRIOR FILING DATE: 2002-05-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 179
;  SOFTWARE: CuraSeqList version 0.1
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;   LENGTH: 3055
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2)..(3055)
US-10-403-676-27

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Db       1143 CGCTCATGGATGAGGCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGG 1202

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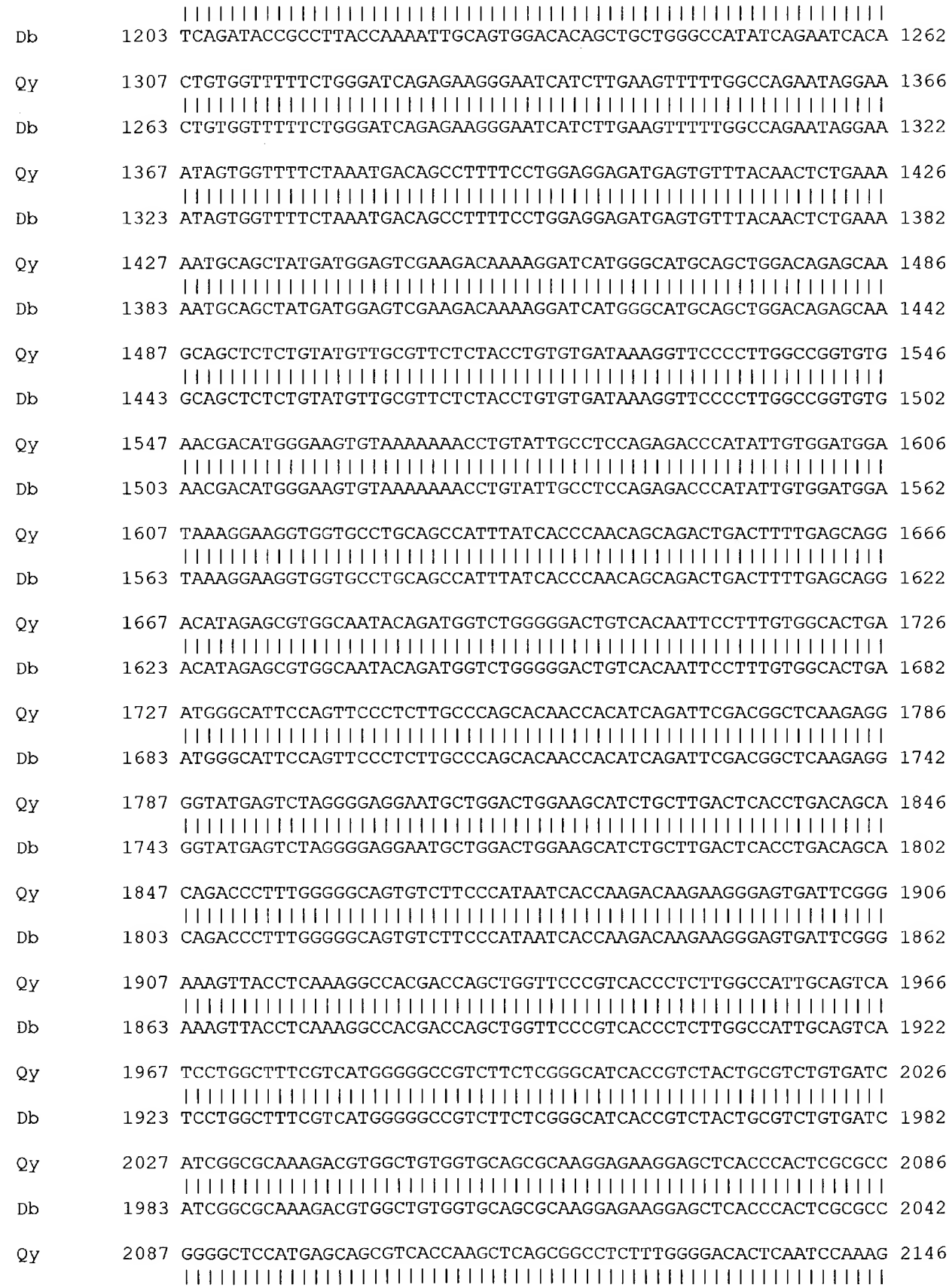
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Db       2283 AGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCT 2342

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Qy       2747 ATAAGAGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAA 2806
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Qy       2807 GAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGG 2866
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2763 GAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGG 2822

Qy       2867 GAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGC 2926
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2823 GAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGC 2882

Qy       2927 CATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGA 2986
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2883 CATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGA 2942
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Qy       2987 CAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCT 3046
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Db       2943 CAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCT 3002

Qy       3047 TTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3090
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Db       3003 TTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3046


RESULT 6
US-10-449-548-27
; Sequence 27, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
;  APPLICANT: Alvarez, Enrique
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Dhanabal, Mohanraj
;  APPLICANT:  Khramtsov, Nikolai V.
;  APPLICANT:  LaRochelle, William J.
;  APPLICANT:  Li, Li
;  APPLICANT:  Lichenstein, Henri
;  APPLICANT:  Ooi, Chean Eng
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
;  FILE REFERENCE: 15966-540CIP2
;  CURRENT APPLICATION NUMBER: US/10/449,548
;  CURRENT FILING DATE:  2003-05-30
;  PRIOR APPLICATION NUMBER: 09/520,781
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/123,667
;  PRIOR FILING DATE: 1999-03-09
;  PRIOR APPLICATION NUMBER: 60/234,082
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: 60/233,798
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 60/174,485
;  PRIOR FILING DATE: 2000-01-04
;  PRIOR APPLICATION NUMBER: 10/403,676
;  PRIOR FILING DATE: 2003-03-31
;  PRIOR APPLICATION NUMBER: 60/371,002
;  PRIOR FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: 60/384,798
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: 60/402,407
;  PRIOR FILING DATE: 2002-08-09
;  PRIOR APPLICATION NUMBER: 60/443,062
;  PRIOR FILING DATE: 2003-01-28
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 27
;   LENGTH: 3055
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
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; NAME/KEY: CDS
; LOCATION: (2)..(3055)
US-10-449-548-27

Query Match 98.2%; Score 3037.6; DB 15; Length 3055;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3040; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy         47 CTGGGGCTGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAA 106
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Db          3 CCGGATCCGGTTTCCCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAA 62

Qy        107 AACAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGC 166
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Db         63 AACAGTATCCGGTGTTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGC 122

Qy        167 TGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TGGACATCCAGATGATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATA 182

Qy        227 TTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGA 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 TTTATACTGTTGATATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGA 242

Qy        287 CATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATG 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 CATGGAAATCTAGACAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATG 302

Qy        347 AGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTG 406
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Db        303 AGTGCCACAACTTTATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTG 362

Qy        407 GAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCG 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GAACTAATGCCTTCAACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCG 422

Qy        467 GGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCAC 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GGGATGAATTCAGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCAC 482

Qy        527 TGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAG 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 TGTTTGCAGATGGAAAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAG 542

Qy        587 TCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAAT 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 TCATTTACCGGAGTCTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAAT 602

Qy        647 GGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCT 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GGTTGAAAGAACCATACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCT 662

Qy        707 TCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTC 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 TCAGGGAAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTC 722

Qy        767 AGGTTTGTAAGAATGATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGT 826
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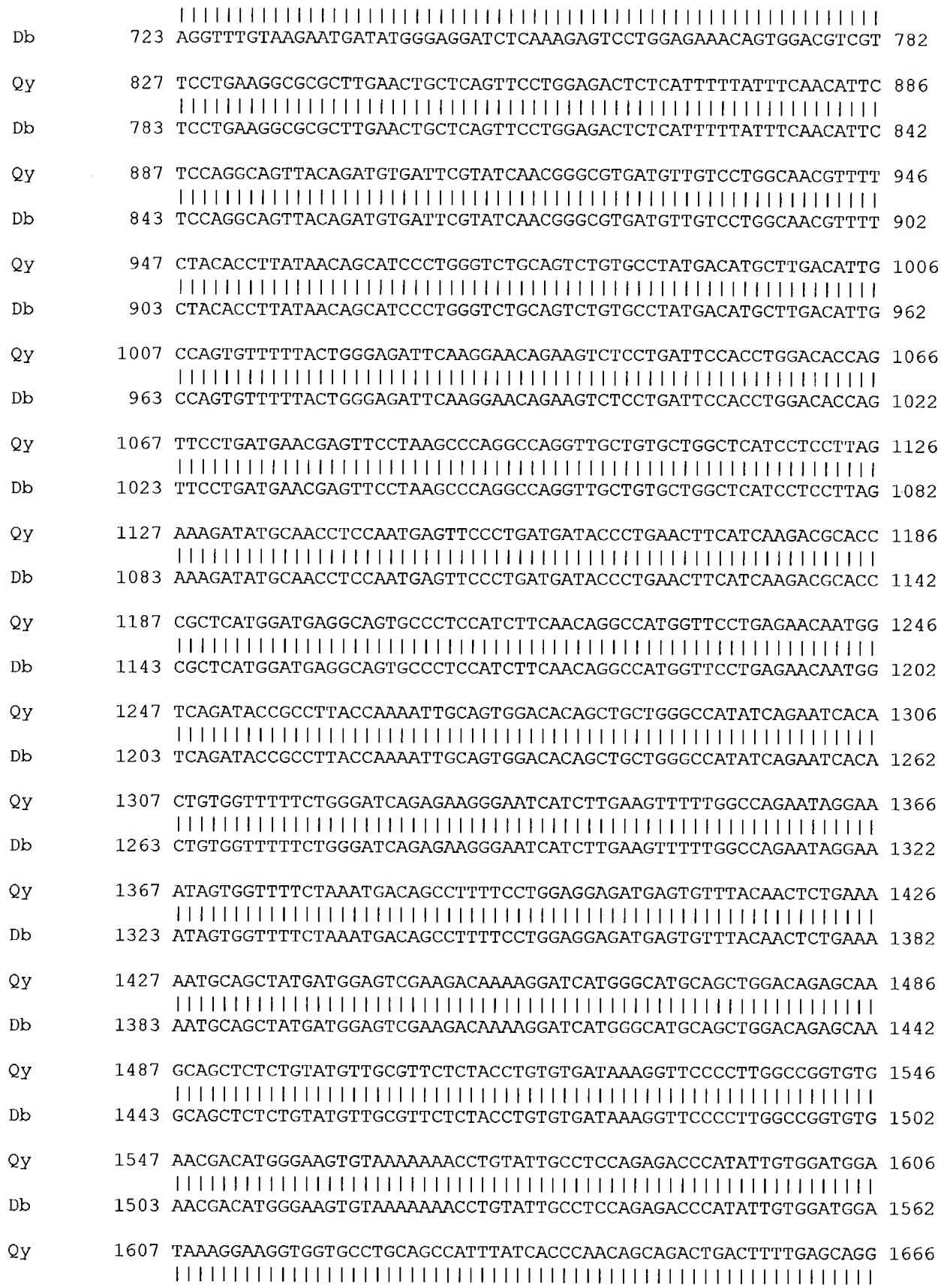

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Db       1563 TAAAGGAAGGTGGTGCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGG 1622

Qy       1667 ACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA 1726
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 ACATAGAGCGTGGCAATACAGATGGTCTGGGGGACTGTCACAATTCCTTTGTGGCACTGA 1682

Qy       1727 ATGGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGG 1786
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1683 ATGGGCATTCCAGTTCCCTCTTGCCCAGCACAACCACATCAGATTCGACGGCTCAAGAGG 1742

Qy       1787 GGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCA 1846
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1743 GGTATGAGTCTAGGGGAGGAATGCTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCA 1802

Qy       1847 CAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGG 1906
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1803 CAGACCCTTTGGGGGCAGTGTCTTCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGG 1862

Qy       1907 AAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCA 1966
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1863 AAAGTTACCTCAAAGGCCACGACCAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCA 1922

Qy       1967 TCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATC 2026
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1923 TCCTGGCTTTCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATC 1982

Qy       2027 ATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCC 2086
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1983 ATCGGCGCAAAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCC 2042

Qy       2087 GGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAG 2146
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2043 GGGGCTCCATGAGCAGCGTCACCAAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAG 2102

Qy       2147 ACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCG 2206
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2103 ACCCAAAGCCGGAGGCCATCCTCACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCG 2162

Qy       2207 GCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCC 2266
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2163 GCAACACGGCCAAGATGCTCATTAAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCC 2222

Qy       2267 CCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCG 2326
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2223 CCACCCCAGAGTCAACCCCAACGCTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCG 2282

Qy       2327 AGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCT 2386
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2283 AGTGGGAGAGGAACCAGAACCTCATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCT 2342

Qy       2387 CCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGG 2446
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2343 CCCCTGTGATTCCCACGGACCTGCCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGG 2402

Qy       2447 TGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGA 2506
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2403 TGGTCCTGCCCATCACGCAGCAGGGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGA 2462
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Qy       2507 GCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCA 2566
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2463 GCGAGGTGGCCCAGATGGCGCTGGAGGACCAGGCCGCCACACTGGAGTATAAGACCATCA 2522

Qy       2567 AGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACA 2626
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2523 AGGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACA 2582

Qy       2627 GCCTGCCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGT 2686
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2583 GCCTGCCCCCCAAAGTTCCACAGCGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGT 2642

Qy       2687 CTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACT 2746
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2643 CTCAGACCGGTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACT 2702

Qy       2747 ATAAGAGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAA 2806
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2703 ATAAGAGGAGCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAA 2762

Qy       2807 GAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGG 2866
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Db       2763 GAAACAACACTAACTCCTCCAATTCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGG 2822

Qy       2867 GAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGC 2926
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2823 GAGACAACCCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGC 2882

Qy       2927 CATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGA 2986
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2883 CATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGA 2942

Qy       2987 CAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCT 3046
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Db       2943 CAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCT 3002

Qy       3047 TTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3090
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Db       3003 TTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3046
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RESULT 7
US-10-393-892-30
; Sequence 30, Application US/10393892
; Publication No. US20030186302A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: COLORECTAL CANCER DIAGNOSTICS
; FILE REFERENCE: CDS 267 US NP
; CURRENT APPLICATION NUMBER: US/10/393,892
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,798
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30

; LENGTH: 4250
; TYPE: DNA
; ORGANISM: human
US-10-393-892-30

Query Match 98.0%; Score 3032; DB 14; Length 4250;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 3093; Conservative 0; Mismatches 0; Indels 51; Gaps 1;

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Db        250 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 309

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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Db        310 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 369

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db        370 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 429

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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Db        430 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 489

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
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Db        490 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 549

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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Db        550 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 609

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Db        610 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 669

Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
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Db        670 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 729

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
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Db        730 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 789

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Db        790 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 849

Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
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Db        850 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 909

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
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Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
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Db        970 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 1029

Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
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Db       1030 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1089

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Db       1090 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1149

Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
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Db       1150 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1209

Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
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Db       1210 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1269

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
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Db       1270 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1329

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1389

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
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Db       1390 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1449

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
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Db       1450 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1509

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1510 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1569

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1629

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Db       1630 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1689

Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
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Db       1690 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1749

Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1750 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1809

Qy       1561 TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
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Db       2650 ATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 2709

Qy       2410 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2769

Qy       2470 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2770 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2829

Qy       2530 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2830 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2889

Qy       2590 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2890 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2949

Qy       2650 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2950 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 3009

Qy       2710 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 2769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 3069

Qy       2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2829
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 3129

Qy       2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 2889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 3189

Qy       2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3190 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 3249

Qy       2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3309

Qy       3010 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3310 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3369

Qy       3070 AAGCCCAATGATGCGTGTACATAA 3093
              |||||||||||||||||||||||
Db       3370 AAGCCCAATGATGCGTGTACATAA 3393
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RESULT 8
US-10-394-382-30
; Sequence 30, Application US/10394382
; Publication No. US20030186303A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Yixin

; TITLE OF INVENTION: COLORECTAL CANCER DIAGNOSTICS
; FILE REFERENCE: CDS 266 US NP
; CURRENT APPLICATION NUMBER: US/10/394,382
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,687
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 4250
;   TYPE: DNA
;   ORGANISM: human
US-10-394-382-30

Query Match 98.0%; Score 3032; DB 14; Length 4250;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 3093; Conservative 0; Mismatches 0; Indels 51; Gaps 1;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 309

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 369

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 429

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 489

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 549

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 609

Qy        361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 669

Qy        421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 729

Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 789

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 849
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Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 909

Qy        661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 969

Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 1029

Qy        781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1089

Qy        841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1149

Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1209

Qy        961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1269

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1329

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1389

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1449

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1509

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1510 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1569

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1629

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1689
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Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1749

Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1750 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1809

Qy       1561 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1810 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1869

Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1870 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1929

Qy       1681 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGA-------------- 1726
             ||||||||||||||||||||||||||||||||||||||||||||||
Db       1930 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT 1989

Qy       1727 ------------------------------------ATGGGCATTCCAGTTCCCTCTTG 1749
                                                    ||||||||||||||||||||||
Db       1990 CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCCTCTTG 2049

Qy       1750 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 1809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2050 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 2109

Qy       1810 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT 1869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2110 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT 2169

Qy       1870 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGAC 1929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2170 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGAC 2229

Qy       1930 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC 1989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2230 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC 2289

Qy       1990 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 2049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2290 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 2349

Qy       2050 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC 2109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC 2409

Qy       2110 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 2169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2410 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 2469

Qy       2170 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 2229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2470 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 2529

Qy       2230 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG 2289
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2530 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG 2589

Qy       2290 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC 2349
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2590 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC 2649

Qy       2350 ATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 2409
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 ATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 2709

Qy       2410 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2469
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2710 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2769

Qy       2470 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2529
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2770 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2829

Qy       2530 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2589
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2830 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2889

Qy       2590 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2649
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2890 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2949

Qy       2650 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2709
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2950 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 3009

Qy       2710 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 2769
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3010 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 3069

Qy       2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2829
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 3129

Qy       2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 2889
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 3189

Qy       2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3190 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 3249

Qy       2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3009
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3309

Qy       3010 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3310 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3369

Qy       3070 AAGCCCAATGATGCGTGTACATAA 3093
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Db       3370 AAGCCCAATGATGCGTGTACATAA 3393


RESULT 9
US-10-120-988-330
; Sequence 330, Application US/10120988
; Publication No. US20030219745A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Goodrich, Ryle
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030219745Alel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 802CON
;  CURRENT APPLICATION NUMBER: US/10/120,988
;  CURRENT FILING DATE:  2002-04-11
;  PRIOR APPLICATION NUMBER: 09/774,528
;  PRIOR FILING DATE: 2001-01-30
;  NUMBER OF SEQ ID NOS: 441
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 330
;   LENGTH: 4280
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (267)..(3410)
US-10-120-988-330

  Query Match             98.0%;  Score 3032;  DB 15;  Length 4280;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 3093;  Conservative    0;  Mismatches    0;  Indels   51;  Gaps    1;

Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 326

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 386

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 446

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 506

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 566

Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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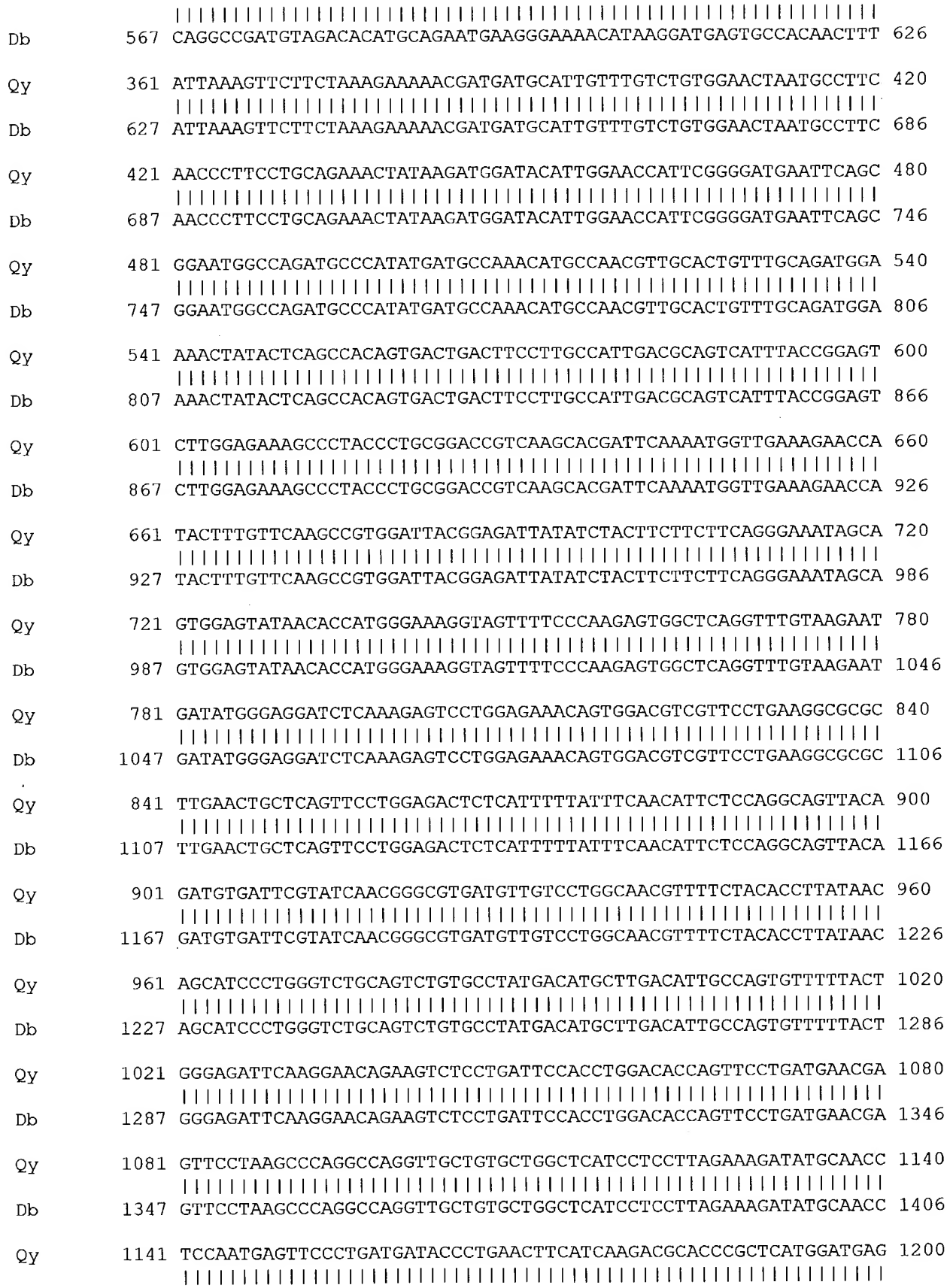

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Db       1467 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1526

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
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Db       1527 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1586

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
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Db       1587 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1646

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Db       1647 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1706

Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
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Db       1707 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1766

Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
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Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
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Qy       1930 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC 1989
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Qy       1990 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 2049
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Qy       2050 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC 2109
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Qy       2110 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 2169
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Qy       2170 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 2229
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Qy       2410 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2469
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Qy       2470 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2529
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US-09-957-187-84
; Sequence 84, Application US/09957187
; Publication No. US20030054514A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard A.
;  APPLICANT:  LaRochelle, William
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
;  FILE REFERENCE: 15966-540 CIP
;  CURRENT APPLICATION NUMBER: US/09/957,187
;  CURRENT FILING DATE:  2000-09-19
;  PRIOR APPLICATION NUMBER: 60/123,667
;  PRIOR FILING DATE: 1999-03-09
;  PRIOR APPLICATION NUMBER: 09/520,781
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/234,082
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: 60/233,798
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 60/174,485
;  PRIOR FILING DATE: 2000-01-04
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;   LENGTH: 4250
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (250)..(3390)
US-09-957-187-84

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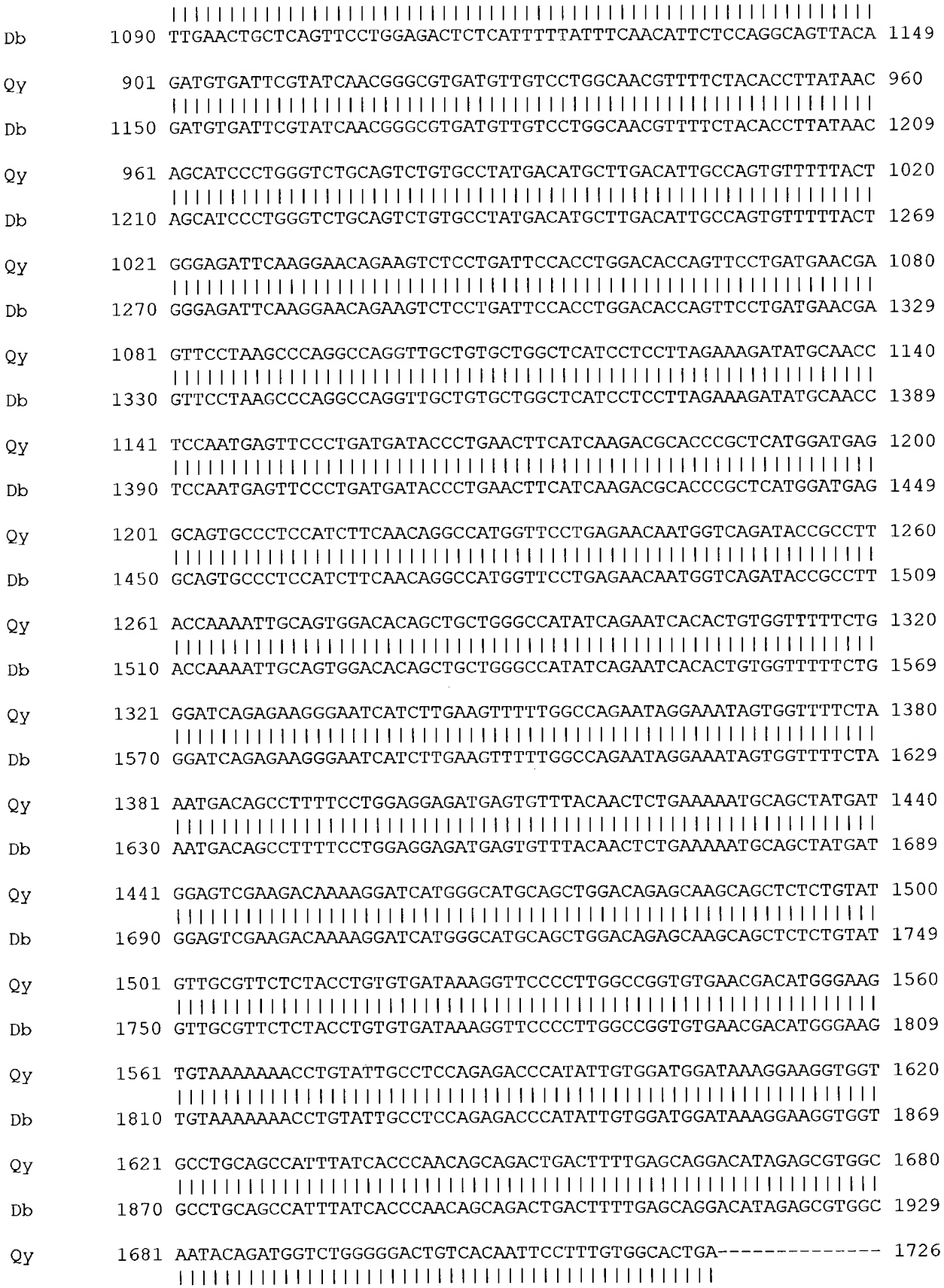

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Db       1990 CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCCTCTTG 2049

Qy       1750 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 1809
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Db       2050 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 2109

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Db       2290 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 2349

Qy       2050 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC 2109
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Qy       2110 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 2169
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RESULT 11
US-10-403-676-13
; Sequence 13, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.

; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 13
; LENGTH: 4250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (250)..(3390)
US-10-403-676-13

Query Match 98.0%; Score 3030.4; DB 12; Length 4250;

Best Local Similarity 98.3%; Pred. No. 0;
Matches 3092; Conservative 0; Mismatches 1; Indels 51; Gaps 1;

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Db        250 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 309

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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Db        310 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATTGCAACTATACAAAACAGTATCCGGTG 369

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Db        370 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 429

Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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Db        430 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 489

Qy        241 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 300
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Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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Db        550 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 609

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Qy        481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
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Db        730 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 789

Qy        541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Qy        601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
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Qy        721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
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Db       1030 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1089

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Qy        901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
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Db       1150 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 1209

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Db       1210 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1269

Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
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Db       1270 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1329

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
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Db       1330 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1389

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
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Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
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Db       1450 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1509

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
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Db       1510 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1569

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
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Db       1570 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1629

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Db       1750 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1809

Qy       1561 TGTAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
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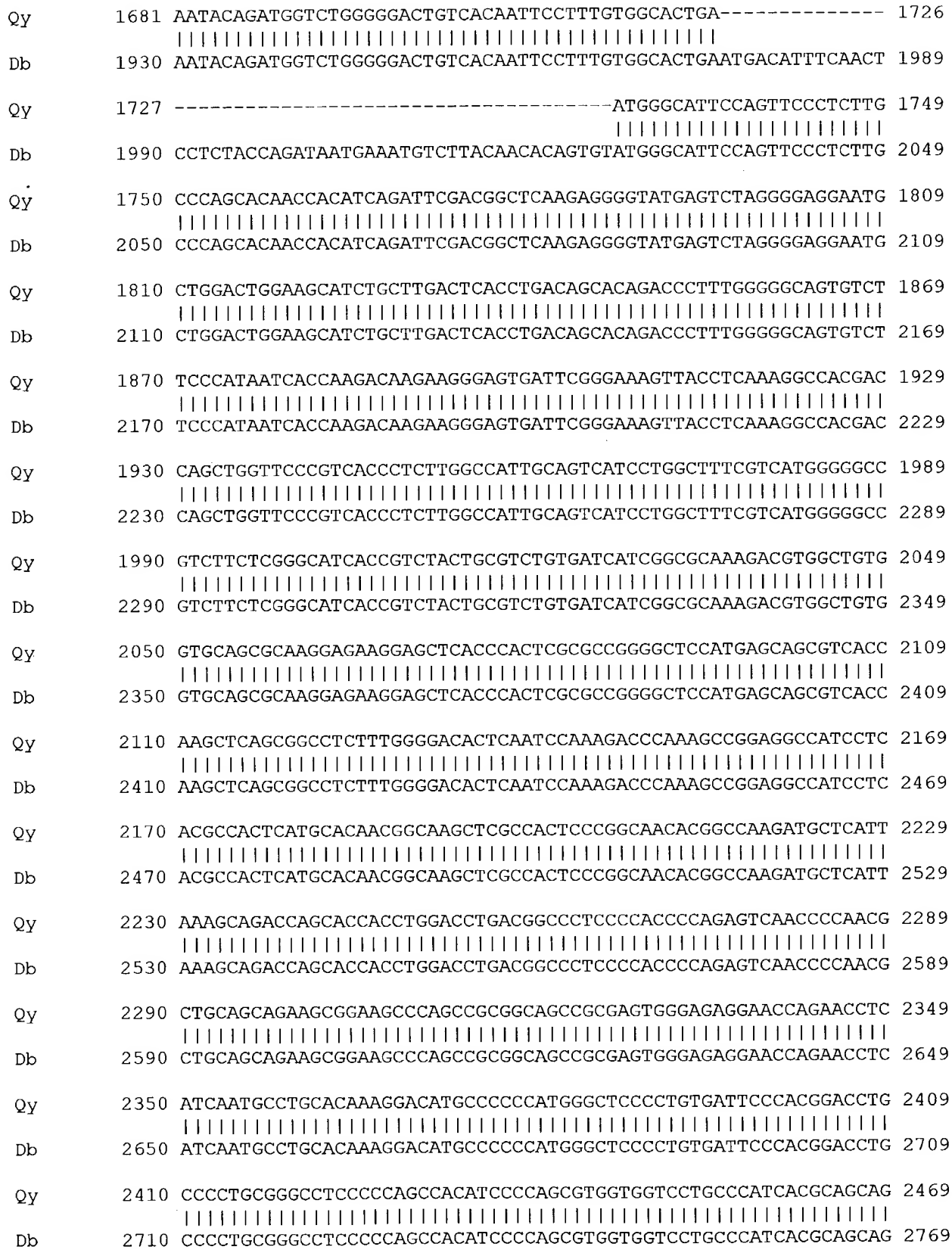

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Db       2770 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2829

Qy       2530 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2589
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Qy       2590 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2649
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Db       2890 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2949

Qy       2650 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2709
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Db       2950 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 3009

Qy       2710 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 2769
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Qy       2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2829
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Db       3070 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 3129

Qy       2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 2889
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Db       3130 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 3189

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RESULT 12
US-10-449-548-13
; Sequence 13, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri

; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 13
;   LENGTH: 4250
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (250)..(3390)
US-10-449-548-13

  Query Match   98.0%; Score 3030.4; DB 15; Length 4250;
  Best Local Similarity   98.3%; Pred. No. 0;
  Matches 3092; Conservative   0; Mismatches   1; Indels   51; Gaps   1;

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Db        250 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 309

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Db        310 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATTGCAACTATACAAAACAGTATCCGGTG 369

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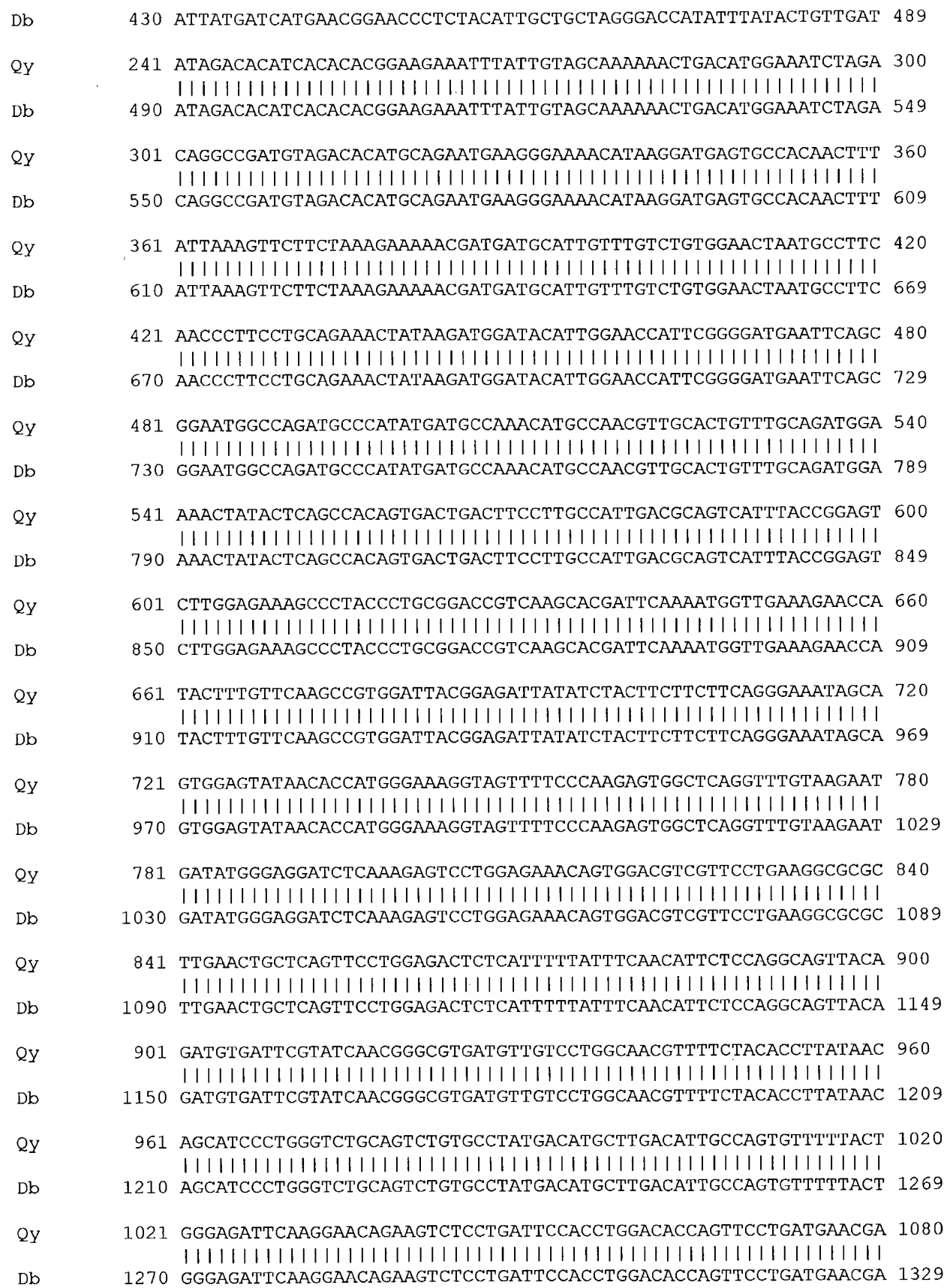
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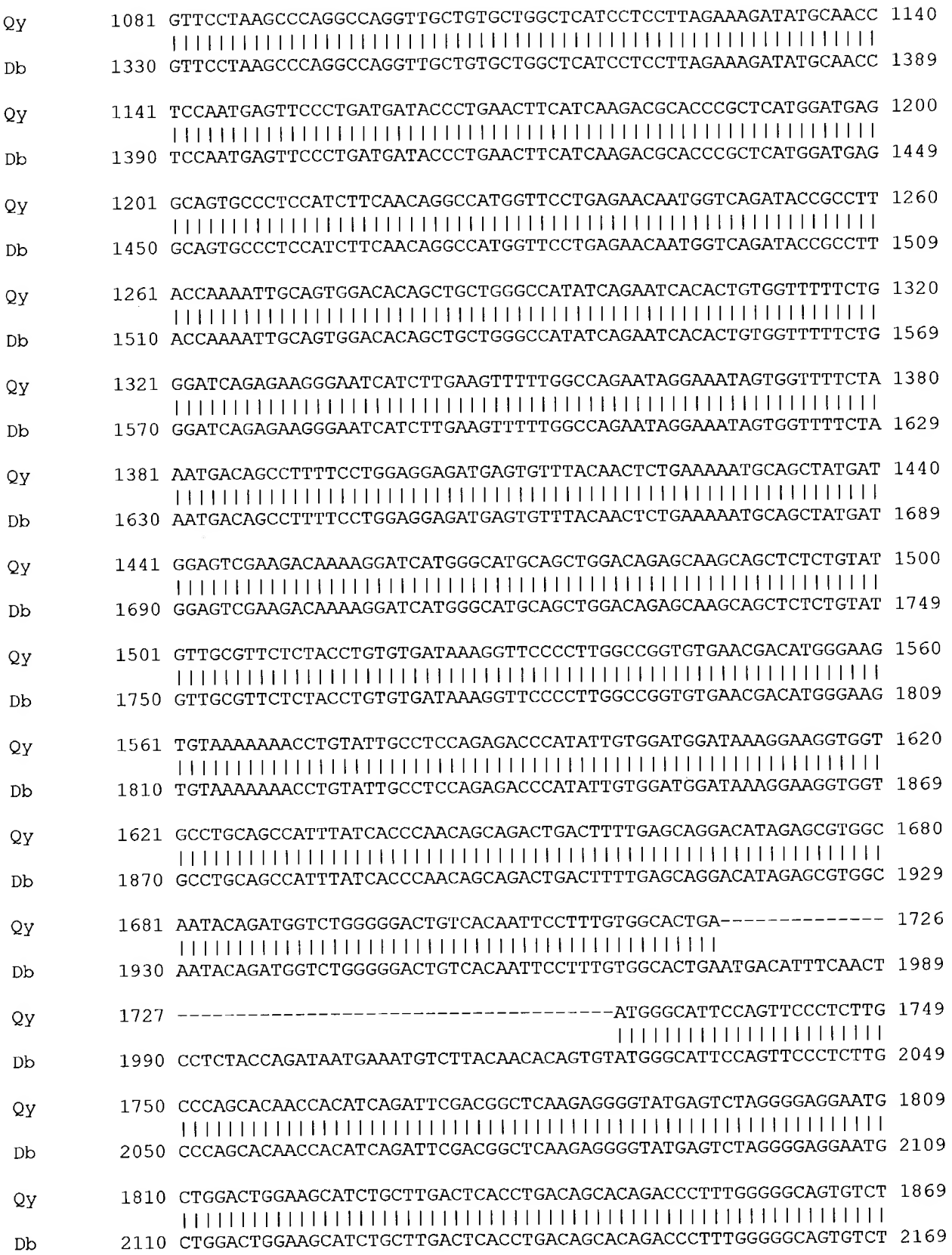
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Db 1810 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1869
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Db 1870 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1929
Qy 1681 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGA---------- 1726
Db 1930 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT 1989
Qy 1727 ----------ATGGGCATTCCAGTTCCCTCTTG 1749
Db 1990 CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCCTCTTG 2049
Qy 1750 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 1809
Db 2050 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 2109
Qy 1810 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT 1869
Db 2110 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT 2169

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Qy       1870 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGAC 1929
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Db       2170 TCCCATAATCACCAAGACAAGAAGGGAGTGATTCGGGAAAGTTACCTCAAAGGCCACGAC 2229

Qy       1930 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC 1989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2230 CAGCTGGTTCCCGTCACCCTCTTGGCCATTGCAGTCATCCTGGCTTTCGTCATGGGGGCC 2289

Qy       1990 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 2049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2290 GTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCAAAGACGTGGCTGTG 2349

Qy       2050 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC 2109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2350 GTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCATGAGCAGCGTCACC 2409

Qy       2110 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 2169
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Db       2410 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 2469

Qy       2170 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 2229
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Db       2470 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 2529

Qy       2230 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG 2289
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Db       2530 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG 2589

Qy       2290 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC 2349
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Db       2590 CTGCAGCAGAAGCGGAAGCCCAGCCGCGGCAGCCGCGAGTGGGAGAGGAACCAGAACCTC 2649

Qy       2350 ATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 2409
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2650 ATCAATGCCTGCACAAAGGACATGCCCCCCATGGGCTCCCCTGTGATTCCCACGGACCTG 2709

Qy       2410 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2469
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Db       2710 CCCCTGCGGGCCTCCCCCAGCCACATCCCCAGCGTGGTGGTCCTGCCCATCACGCAGCAG 2769

Qy       2470 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2529
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Db       2770 GGCTACCAGCATGAGTACGTGGACCAGCCCAAAATGAGCGAGGTGGCCCAGATGGCGCTG 2829

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Db       2830 GAGGACCAGGCCGCCACACTGGAGTATAAGACCATCAAGGAACATCTCAGCAGCAAGAGT 2889

Qy       2590 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2649
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Db       2890 CCCAACCATGGGGTGAACCTTGTGGAGAACCTGGACAGCCTGCCCCCCAAAGTTCCACAG 2949

Qy       2650 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2709
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Db       2950 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 3009

Qy       2710 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 2769
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Db       3010 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 3069

Qy       2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2829
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3070 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 3129

Qy       2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 2889
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3130 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 3189

Qy       2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
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Db       3190 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 3249

Qy       2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3009
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3250 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3309

Qy       3010 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3310 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3369

Qy       3070 AAGCCCAATGATGCGTGTACATAA 3093
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Db       3370 AAGCCCAATGATGCGTGTACATAA 3393
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RESULT 13
US-10-403-676-47
; Sequence 47, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 47
; LENGTH: 3165
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(3153)
US-10-403-676-47

Query Match 97.8%; Score 3025.8; DB 12; Length 3165;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3088; Conservative 0; Mismatches 2; Indels 51; Gaps 1;

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Qy          1 ATGAGGTCAGAAGCCTTGCTGCTATATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 60
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         13 ATGAGGTCAGAAGCCTTGCTGCTGTATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 72

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 132

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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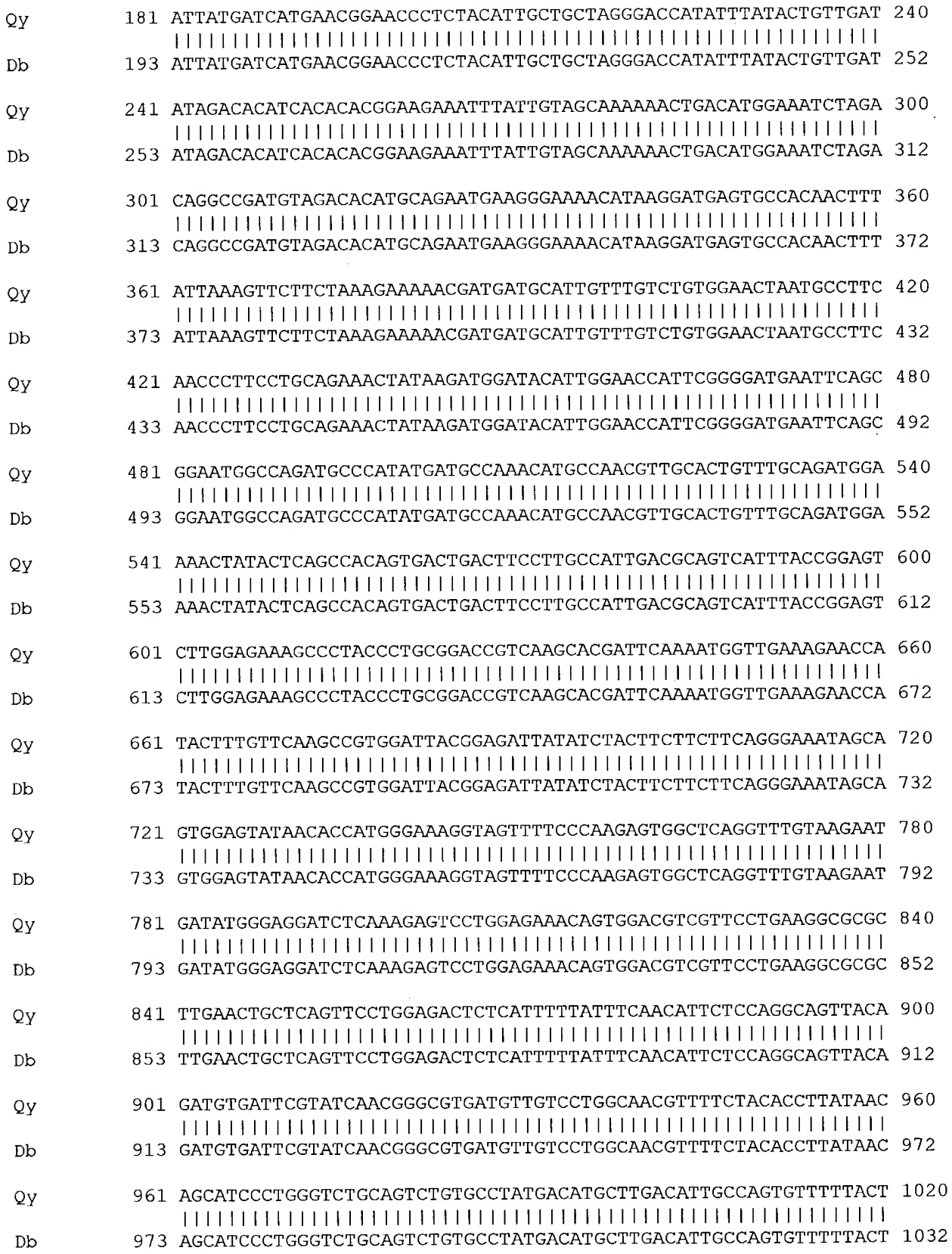
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Db 253 ATAGACACATCACACACGGAAGAAATTTATTGTAGCAAAAAACTGACATGGAAATCTAGA 312
Qy 301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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Qy 361 ATTAAAGTTCTTCTAAAGAAAAACGATGATGCATTGTTTGTCTGTGGAACTAATGCCTTC 420
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Qy 421 AACCCTTCCTGCAGAAACTATAAGATGGATACATTGGAACCATTCGGGGATGAATTCAGC 480
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Qy 481 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 540
Db 493 GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 552
Qy 541 AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 600
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Qy 601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
Db 613 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 672
Qy 661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
Db 673 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 732
Qy 721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
Db 733 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 792
Qy 781 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 840
Db 793 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 852
Qy 841 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 900
Db 853 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 912
Qy 901 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 960
Db 913 GATGTGATTCGTATCAACGGGCGTGATGTTGTCCTGGCAACGTTTTCTACACCTTATAAC 972
Qy 961 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1020
Db 973 AGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTTACT 1032

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Qy       1021 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1080
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Db       1033 GGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAACGA 1092

Qy       1081 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 GTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCAACC 1152

Qy       1141 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 TCCAATGAGTTCCCTGATGATACCCTGAACTTCATCAAGACGCACCCGCTCATGGATGAG 1212

Qy       1201 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1260
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Db       1213 GCAGTGCCCTCCATCTTCAACAGGCCATGGTTCCTGAGAACAATGGTCAGATACCGCCTT 1272

Qy       1261 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1320
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Db       1273 ACCAAAATTGCAGTGGACACAGCTGCTGGGCCATATCAGAATCACACTGTGGTTTTTCTG 1332

Qy       1321 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1380
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Db       1333 GGATCAGAGAAGGGAATCATCTTGAAGTTTTTGGCCAGAATAGGAAATAGTGGTTTTCTA 1392

Qy       1381 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1440
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Db       1393 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTTACAACTCTGAAAAATGCAGCTATGAT 1452

Qy       1441 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1500
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Db       1453 GGAGTCGAAGACAAAAGGATCATGGGCATGCAGCTGGACAGAGCAAGCAGCTCTCTGTAT 1512

Qy       1501 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1560
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Db       1513 GTTGCGTTCTCTACCTGTGTGATAAAGGTTCCCCTTGGCCGGTGTGAACGACATGGGAAG 1572

Qy       1561 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCATATTGTGGATGGATAAAGGAAGGTGGT 1620
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Db       1573 TGTAAAAAAAACCTGTATTGCCTCCAGAGACCCGTATTGTGGATGGATAAAGGAAGGTGGT 1632

Qy       1621 GCCTGCAGCCATTTATCACCCAACAGCAGACTGACTTTTGAGCAGGACATAGAGCGTGGC 1680
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Qy       1681 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGA---------------- 1726
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Db       1693 AATACAGATGGTCTGGGGGGACTGTCACAATTCCTTTGTGGCACTGAATGACATTTCAACT 1752

Qy       1727 ------------------------------------ATGGGCATTCCAGTTCCCTCTTG 1749
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Db       1753 CCTCTACCAGATAATGAAATGTCTTACAACACAGTGTATGGGCATTCCAGTTCCCTCTTG 1812

Qy       1750 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 1809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1813 CCCAGCACAACCACATCAGATTCGACGGCTCAAGAGGGGTATGAGTCTAGGGGAGGAATG 1872

Qy       1810 CTGGACTGGAAGCATCTGCTTGACTCACCTGACAGCACAGACCCTTTGGGGGCAGTGTCT 1869
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Db       2713 CGGGAGGCCTCCCTGGGTCCCCCGGGAGCCTCCCTGTCTCAGACCGGTCTAAGCAAGCGG 2772

Qy       2710 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 2769
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Db       2773 CTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGAGCTACCCCACGAAC 2832

Qy       2770 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2829
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Db       2833 TCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACACTAACTCCTCCAAT 2892

Qy       2830 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 2889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2893 TCCTCTCACCTCTCCAGAAACCAGAGCTTTGGCAGGGGAGACAACCCGCCGCCCGCCCCG 2952

Qy       2890 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 2949
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Db       2953 CAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTC 3012

Qy       2950 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3009
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Db       3013 TCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACG 3072

Qy       3010 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3069
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Db       3073 CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATG 3132

Qy       3070 AAGCCCAATGATGCGTGTACA 3090
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Db       3133 AAGCCCAATGATGCGTGTACA 3153
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RESULT 14
US-10-449-548-47
; Sequence 47, Application US/10449548
; Publication No. US20040018977A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Anderson, David W.
; APPLICANT: Dhanabal, Mohanraj
; APPLICANT: Khramtsov, Nikolai V.
; APPLICANT: LaRochelle, William J.
; APPLICANT: Li, Li
; APPLICANT: Lichenstein, Henri
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: SEMAPHORIN-LIKE PROTEINS AND METHODS OF USING SAME
; FILE REFERENCE: 15966-540CIP2
; CURRENT APPLICATION NUMBER: US/10/449,548
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 60/234,082
; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; PRIOR APPLICATION NUMBER: 10/403,676
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/384,798
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/402,407
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/443,062
; PRIOR FILING DATE: 2003-01-28
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 47
;   LENGTH: 3165
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (13)..(3153)
US-10-449-548-47

Query Match 97.8%; Score 3025.8; DB 15; Length 3165;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3088; Conservative 0; Mismatches 2; Indels 51; Gaps 1;

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Db         13 ATGAGGTCAGAAGCCTTGCTGCTGTATTTCACACTGCTACACTTTGCTGGGGCTGGTTTC 72

Qy         61 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 120
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Db         73 CCAGAAGATTCTGAGCCAATCAGTATTTCGCATGGCAACTATACAAAACAGTATCCGGTG 132

Qy        121 TTTGTGGGCCACAAGCCAGGACGGAACACCACACAGAGGCACAGGCTGGACATCCAGATG 180
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Qy        181 ATTATGATCATGAACGGAACCCTCTACATTGCTGCTAGGGACCATATTTATACTGTTGAT 240
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Qy        301 CAGGCCGATGTAGACACATGCAGAATGAAGGGAAAACATAAGGATGAGTGCCACAACTTT 360
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Qy       601 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 660
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Db       613 CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 672

Qy       661 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 720
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Db       673 TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 732

Qy       721 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 780
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Db       733 GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 792

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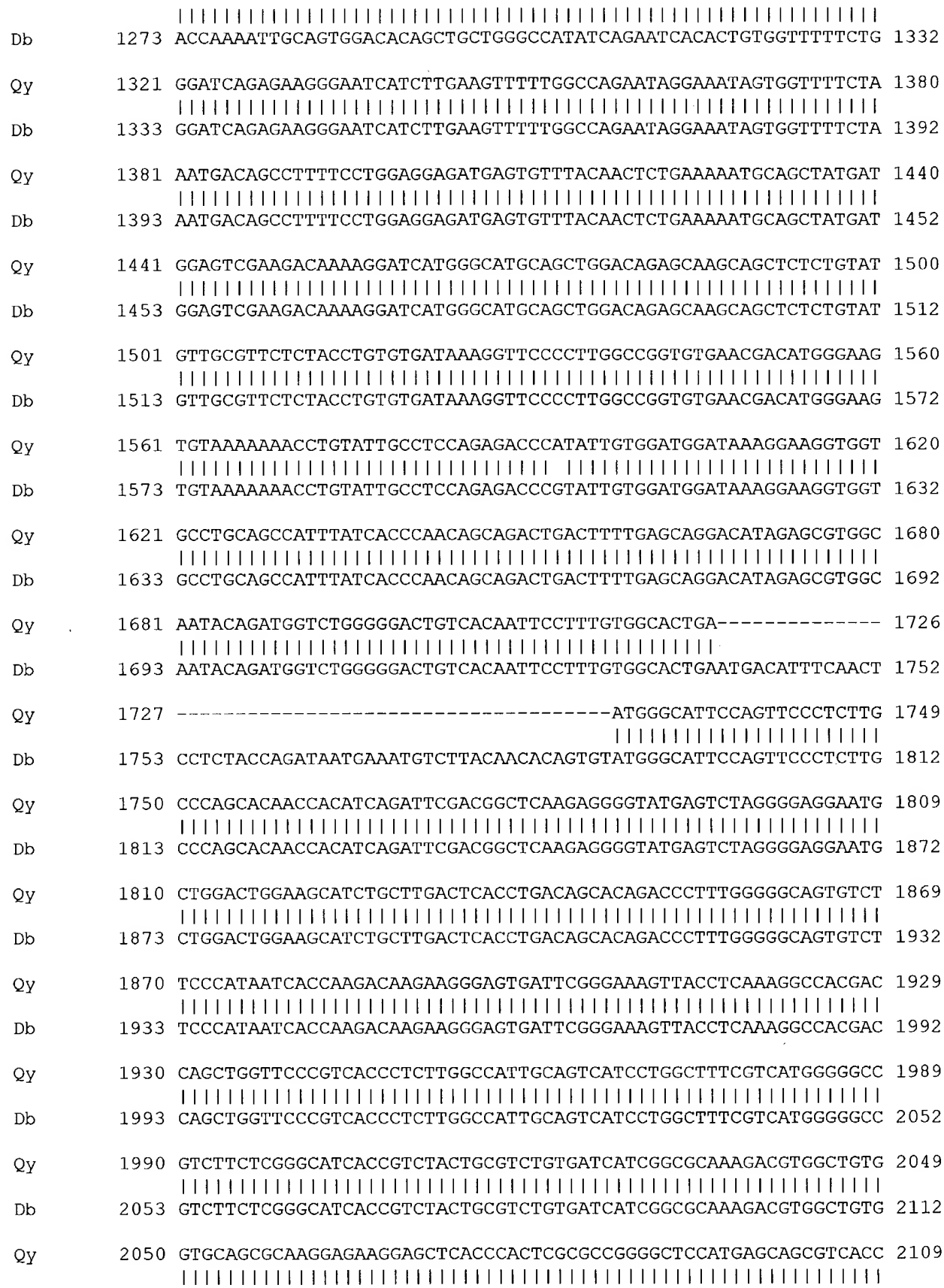

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Db       2173 AAGCTCAGCGGCCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAGGCCATCCTC 2232

Qy       2170 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 2229
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Db       2233 ACGCCACTCATGCACAACGGCAAGCTCGCCACTCCCGGCAACACGGCCAAGATGCTCATT 2292

Qy       2230 AAAGCAGACCAGCACCACCTGGACCTGACGGCCCTCCCCACCCCAGAGTCAACCCCAACG 2289
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RESULT 15
US-10-403-676-17
; Sequence 17, Application US/10403676
; Publication No. US20040029150A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Grosse, William M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: LaRochelle, William J.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE
; FILE REFERENCE: 21402-573B
; CURRENT APPLICATION NUMBER: US/10/403,676
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/123,667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520,781
; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 09/957,187
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/371,002
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/604,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/370,381
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,297
; PRIOR FILING DATE: 2002-05-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 17
;   LENGTH: 3106
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;   FEATURE:
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US-10-403-676-17

  Query Match   96.2%; Score 2975; DB 12; Length 3106;
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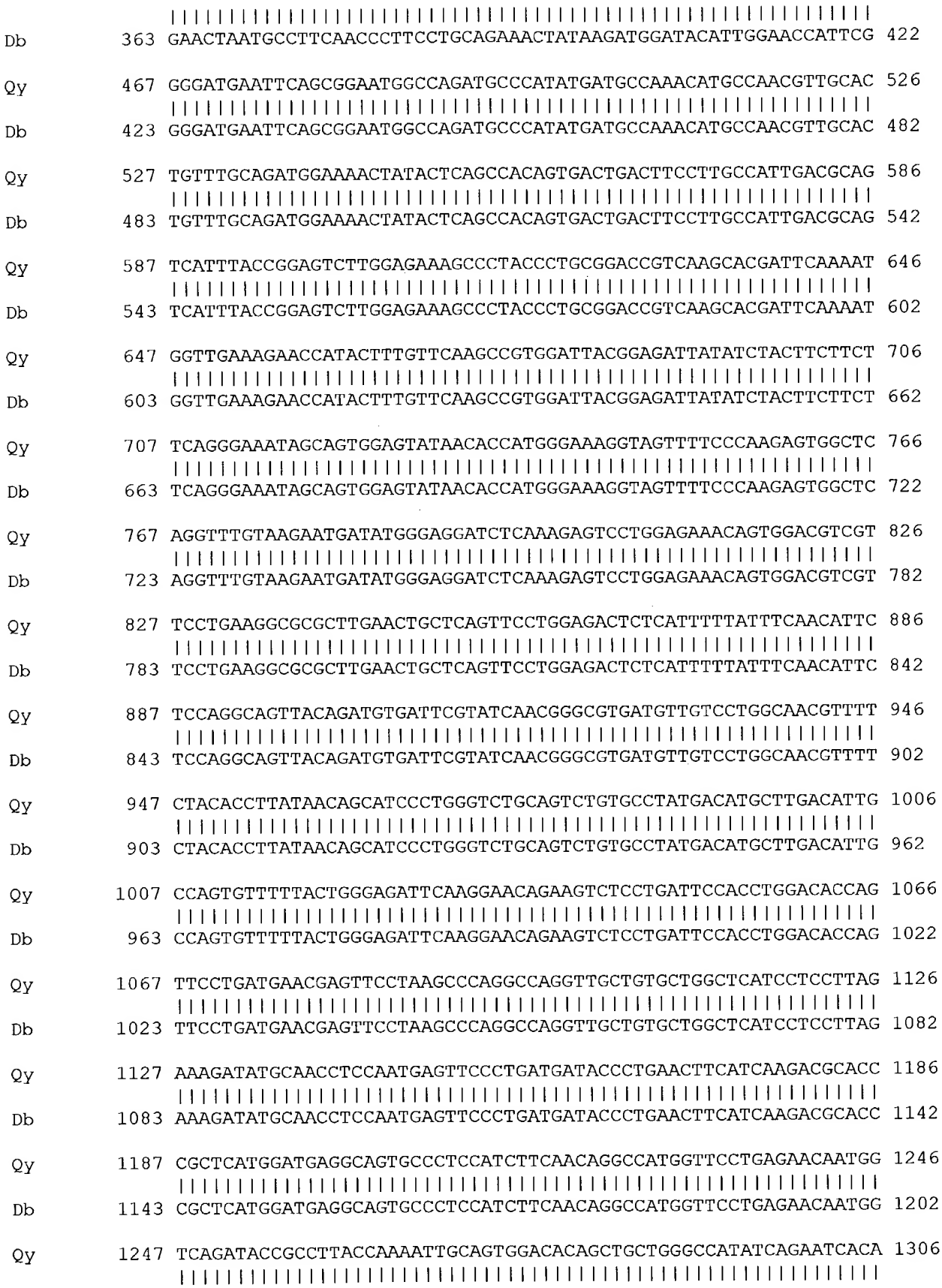

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Qy       1976 TCGTCATGGGGGCCGTCTTCTCGGGCATCACCGTCTACTGCGTCTGTGATCATCGGCGCA 2035
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Db       2043 AAGACGTGGCTGTGGTGCAGCGCAAGGAGAAGGAGCTCACCCACTCGCGCCGGGGCTCCA 2102
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Qy       2696 GTCTAAGCAAGCGGCTGGAAATGCACCACTCCTCTTCCTACGGGGTTGACTATAAGAGGA 2755
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Qy       2756 GCTACCCCACGAACTCGCTCACGAGAAGCCACCAGGCCACCACTCTCAAAAGAAACAACA 2815
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Qy       2876 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 2935
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2936 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGG 2995
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Qy       2996 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 3055
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3056 TTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3090
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